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<110> Seishi KATO  
 Chikashi EGUCHI  
 Mihoro SAEKI

<120> Human Proteins and cDNAs thereof

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Ala Met Ala Pro Thr Ser Pro Gln Ile  
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Figure 1 consists of 12 sub-graphs, labeled (a) through (l), each showing the time course of a different physiological parameter over a 10-minute period. The x-axis for all graphs is 'Time (min)' ranging from 0 to 10. The y-axis represents the value of the parameter. Each graph shows a baseline period (from 0 to 10 minutes) and a 10-minute intervention period (from 10 to 20 minutes). The parameters are: (a) HR (b/min), (b) BP (mmHg), (c) SV (ml), (d) CO (l/min), (e) SVR (mmHg/l/min), (f) PVR (mmHg/l/min), (g) P (mmHg), (h) Vt (ml), (i) VE (l/min), (j) Pao2 (mmHg), (k) Pao2/FiO2, and (l) P/F ratio. The graphs show that HR, BP, SV, CO, SVR, PVR, P, Vt, VE, Pao2, Pao2/FiO2, and P/F ratio all increase during the intervention period.

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General information	
Study	1997-1998
Location	USA
Study design	Case-control
Study population	1000 cases of acute myocardial infarction (AMI) and 1000 controls
Exposure assessment	Self-reported
Outcome assessment	Medical records
Follow-up period	1 year
Loss to follow-up	10%
Response rate	80%
Statistical methods	Logistic regression
Significance level	0.05
Confidence interval	95%
Results	OR 1.5, 95% CI 1.2-1.8
Conclusion	Physical activity is associated with a lower risk of AMI

Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
Male	50.2 (10.5)
Female	51.5 (11.2)
Marital status	
Married	78.5%
Single	21.5%
Education (years)	Mean (SD)
Male	12.5 (2.5)
Female	11.8 (2.8)
Occupation	
Professional	35.2%
Managerial	28.7%
Technical	15.3%
Service	10.8%
Unemployed	9.0%
Income (USD/month)	Mean (SD)
Male	1,200 (300)
Female	1,150 (280)
Health insurance	
Yes	92.5%
No	7.5%
Smoking status	
Smoker	25.3%
Non-smoker	74.7%
Alcohol consumption	
Yes	12.1%
No	87.9%
Family size	Mean (SD)
Male	3.2 (1.5)
Female	3.1 (1.4)
Urban/rural	
Urban	65.4%
Rural	34.6%

[illegible]

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 Ala Gly Gly Arg Pro Pro Trp Pro Val Ser Gly Val Leu Gly Ser Arg  
 20 25 30  
 Val Cys Gly Pro Leu Tyr Ser Thr Ser Pro Ala Gly Pro Gly Arg Ala  
 35 40 45  
 Ala Ser Leu Pro Arg Lys Gly Ala Gln Leu Glu Leu Glu Glu Met Leu  
 50 55 60  
 Val Pro Arg Lys Met Ser Val Ser Pro Leu Glu Ser Trp Leu Thr Ala  
 65 70 75 80  
 Arg Cys Phe Leu Pro Arg Leu Asp Thr Gly Thr Ala Gly Thr Val Ala  
 85 90 95  
 Pro Pro Gln Ser Tyr Gln Cys Pro Pro Ser Gln Ile Gly Glu Gly Ala  
 100 105 110  
 Glu Gln Gly Asp Glu Gly Val Ala Asp Ala Pro Gln Ile Gln Cys Lys  
 115 120 125  
 Asn Val Leu Lys Ile Arg Arg Arg Lys Met Asn His His Lys Tyr Arg  
 130 135 140  
 Lys Leu Val Lys Lys Thr Arg Phe Leu Arg Arg Lys Val Gln Glu Gly  
 145 150 155 160  
 Arg Leu Arg Arg Lys Gln Ile Lys Phe Glu Lys Asp Leu Arg Arg Ile  
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gtt tca tcc gcc ctg aaa tct tcc cga tcg tta ata act cct cag gtc 98  
 Val Ser Ser Ala Leu Lys Ser Ser Arg Ser Leu Ile Thr Pro Gln Val  
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cct gcc tgc aca ggg ttt ttt ctt agt ttg ttg cct aag agt aca cca 146  
 Pro Ala Cys Thr Gly Phe Phe Leu Ser Leu Leu Pro Lys Ser Thr Pro  
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aat gtg aca tcc ttt cac caa tat aga tta ctt cat acc aca ttg tca 194  
 Asn Val Thr Ser Phe His Gln Tyr Arg Leu Leu His Thr Thr Leu Ser  
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agg aaa gga cta gaa gaa ttt ttt gat gac cca aaa aac tgg ggg caa 242  
 Arg Lys Gly Leu Glu Glu Phe Phe Asp Asp Pro Lys Asn Trp Gly Gln  
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gaa aaa gta aaa tct gga gca gca tgg acc tgt cag caa cta agg aac 290  
 Glu Lys Val Lys Ser Gly Ala Ala Trp Thr Cys Gln Gln Leu Arg Asn  
                           80                          85                          90

aaa agt aat gaa gat tta cac aaa ctt tgg tat gtc tta ctg aaa gaa 338  
 Lys Ser Asn Glu Asp Leu His Lys Leu Trp Tyr Val Leu Leu Lys Glu  
                   95                          100                          105

aga aac atg ctt cta acc cta gag cag gag gcc aag cgg cag aga ttg 386  
 Arg Asn Met Leu Leu Thr Leu Glu Gln Glu Ala Lys Arg Gln Arg Leu  
                   110                          115                          120

cca atg cca agt cca gag cgg tta gat aag gta gta gat tcc atg gat 434  
 Pro Met Pro Ser Pro Glu Arg Leu Asp Lys Val Val Asp Ser Met Asp  
                   125                          130                          135                          140

gca tta gat aaa gtt gtc cag gaa aga gaa gat gcc cta agg ctt ctt 482  
 Ala Leu Asp Lys Val Val Gln Glu Arg Glu Asp Ala Leu Arg Leu Leu  
                           145                          150                          155

cag act ggt caa gaa aga gct aga cct ggt gct tgg aga aga gac atc 530  
 Gln Thr Gly Gln Glu Arg Ala Arg Pro Gly Ala Trp Arg Arg Asp Ile  
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ttt gga aga atc atc tgg cac aag ttc aag cag tgg gtt ata cct tgg 578



09350688-092704

Glu Arg Ala Arg Pro Gly Ala Trp Arg Arg Asp Ile Phe Gly Arg Ile  
165 170 175

Ile Trp His Lys Phe Lys Gln Trp Val Ile Pro Trp His Leu Asn Lys  
180 185 190

Arg Tyr Asn Arg Lys Arg Phe Phe Ala Leu Pro Tyr Val Asp His Phe  
195 200 205

Leu Arg Leu Glu Arg Glu Lys Arg Ala Arg Ile Lys Ala Arg Lys Glu  
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1 5 10

act gag aag aag ttc tta agg aaa cag att aaa gcc aag cat act ttg 218  
Thr Glu Lys Lys Phe Leu Arg Lys Gln Ile Lys Ala Lys His Thr Leu  
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ctg aga cat gaa ggc att gag aca gta tcc tat gcc act cag agc ctg 266  
Leu Arg His Glu Gly Ile Glu Thr Val Ser Tyr Ala Thr Gln Ser Leu  
30 35 40 45

gtt gtt gcc aat ggt ggt ttg ggt aat ggt gtg agt cgg aac cag ctg 314  
Val Val Ala Asn Gly Gly Leu Gly Asn Gly Val Ser Arg Asn Gln Leu  
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ctc ccg gtt tta gag aaa tgt gga ctg gtg gat gct ctc tta atg cca 362  
Leu Pro Val Leu Glu Lys Cys Gly Leu Val Asp Ala Leu Leu Met Pro  
65 70 75

cct aac aag ccg tac tca ttt gca aga tac aga act aca gaa gaa tct 410  
Pro Asn Lys Pro Tyr Ser Phe Ala Arg Tyr Arg Thr Thr Glu Glu Ser  
80 85 90

aag aga gcc tat gtt acc ctc aat gga aaa gaa gta gtg gat gat tta	458
Lys Arg Ala Tyr Val Thr Leu Asn Gly Lys Glu Val Val Asp Asp Leu	
95 100 105	
gga caa aag atc act ctg tat ttg aat ttt gtg gaa aaa gtg cag tgg	506
Gly Gln Lys Ile Thr Leu Tyr Leu Asn Phe Val Glu Lys Val Gln Trp	
110 115 120 125	
aag gag ttg agg cct caa gcc tta cca cca gga ctc atg gta gta gaa	554
Lys Glu Leu Arg Pro Gln Ala Leu Pro Pro Gly Leu Met Val Val Glu	
130 135 140	
gaa ata att tct tct gag gag gag aaa atg ctt ttg gaa agt gtt gat	602
Glu Ile Ile Ser Ser Glu Glu Glu Lys Met Leu Leu Glu Ser Val Asp	
145 150 155	
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Trp Thr Glu Asp Thr Asp Asn Gln Asn Ser Gln Lys Ser Leu Lys His	
160 165 170	
aga aga gta aag cat ttt ggt tat gag ttc cac tat gag aac aac aat	698
Arg Arg Val Lys His Phe Gly Tyr Glu Phe His Tyr Glu Asn Asn Asn	
175 180 185	
gta gat aaa gat aag cca tta tct ggg ggt ctt cct gac att tgt gaa	746
Val Asp Lys Asp Lys Pro Leu Ser Gly Gly Leu Pro Asp Ile Cys Glu	
190 195 200 205	
agc ttt ttg gag aaa tgg ttg agg aaa ggt tac att aaa cat aaa cct	794
Ser Phe Leu Glu Lys Trp Leu Arg Lys Gly Tyr Ile Lys His Lys Pro	
210 215 220	
gat caa atg acc ata aat cag tat gaa cct ggg caa gga att ccc gct	842
Asp Gln Met Thr Ile Asn Gln Tyr Glu Pro Gly Gln Gly Ile Pro Ala	
225 230 235	
cat att gac aca cat tcc gct ttt gag gat gag atc gtt tct ctc agt	890
His Ile Asp Thr His Ser Ala Phe Glu Asp Glu Ile Val Ser Leu Ser	
240 245 250	
ttg ggg tca gag att gtc atg gat ttt aag cac cca gat ggc att gca	938
Leu Gly Ser Glu Ile Val Met Asp Phe Lys His Pro Asp Gly Ile Ala	
255 260 265	
gtg cca gtt atg ttg cct cgt cgg agt ttg ctg gtg atg aca gga gaa	986
Val Pro Val Met Leu Pro Arg Arg Ser Leu Leu Val Met Thr Gly Glu	
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Ser Arg Tyr Leu Trp Thr His Gly Ile Thr Cys Arg Lys Phe Asp Thr	
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Val Gln Ala Ser Glu Ser Leu Lys Ser Gly Ile Ile Thr Ser Asp Val	
305 310 315	

gga gac tta act tta agc aag agg gga cta cga aca tca ttt aca ttt	1130
Gly Asp Leu Thr Leu Ser Lys Arg Gly Leu Arg Thr Ser Phe Thr Phe	
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agg aaa gtg agg caa aca cct tgt aac tgt agt tac ccg ttg gtc tgt	1178
Arg Lys Val Arg Gln Thr Pro Cys Asn Cys Ser Tyr Pro Leu Val Cys	
335 340 345	
gat agc cag agg aaa gag act ccc ccc tca ttt cca gag agt gat aaa	1226
Asp Ser Gln Arg Lys Glu Thr Pro Pro Ser Phe Pro Glu Ser Asp Lys	
350 355 360 365	
gaa gcc tca cgg ctg gag caa gag tac gtc cat cag gtt tat gaa gag	1274
Glu Ala Ser Arg Leu Glu Gln Glu Tyr Val His Gln Val Tyr Glu Glu	
370 375 380	
att gct ggg cac ttc agc agc aca aga cat acc cct tgg ccg cac att	1322
Ile Ala Gly His Phe Ser Ser Thr Arg His Thr Pro Trp Pro His Ile	
385 390 395	
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Val Glu Phe Leu Lys Ala Leu Pro Ser Gly Ser Ile Val Ala Asp Ile	
400 405 410	
gga tgt ggt aat gga aag tat ctt ggc atc aat aag gag tta tat atg	1418
Gly Cys Gly Asn Gly Lys Tyr Leu Gly Ile Asn Lys Glu Leu Tyr Met	
415 420 425	
gag cgt aga gtg gca gct ctc caa gaa att gtt cga ctc ctg aga cca	1466
Glu Arg Arg Val Ala Ala Leu Gln Glu Ile Val Arg Leu Leu Arg Pro	
430 435 440 445	
ggt ggg aag gca ctc att tat gtc tgg gca atg gaa caa gaa tat aat	1514
Gly Gly Lys Ala Leu Ile Tyr Val Trp Ala Met Glu Gln Glu Tyr Asn	
450 455 460	
aag cag aag tcc aag tat ctt aga gga aac aga aat agc caa gga aag	1562
Lys Gln Lys Ser Lys Tyr Leu Arg Gly Asn Arg Asn Ser Gln Gly Lys	
465 470 475	
aaa gag gag atg aac agt gat acc tca gtg cag agg tca ctt gtg gag	1610
Lys Glu Glu Met Asn Ser Asp Thr Ser Val Gln Arg Ser Leu Val Glu	
480 485 490	
caa atg cgt gac atg ggc agt cga gac tcg gca tct tct gtc ccc cgc	1658
Gln Met Arg Asp Met Gly Ser Arg Asp Ser Ala Ser Ser Val Pro Arg	
495 500 505	
att aat gac tct cag gaa gga gga tgt aat tca agg caa gtt tct aat	1706
Ile Asn Asp Ser Gln Glu Gly Gly Cys Asn Ser Arg Gln Val Ser Asn	
510 515 520 525	
tcc aag ctg cct gtt cat gtt aac agg act tct ttt tat tct caa gat	1754
Ser Lys Leu Pro Val His Val Asn Arg Thr Ser Phe Tyr Ser Gln Asp	
530 535 540	
gta ctg gtt ccc tgg cac ctt aag gga aat cct gat aaa ggc aaa cct	1802

Val Leu Val Pro Trp His Leu Lys Gly Asn Pro Asp Lys Gly Lys Pro  
545 550 555

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Val Glu Pro Phe Gly Pro Ile Gly Ser Gln Asp Pro Ser Pro Val Phe  
560 565 570

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575 580 585

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Arg Thr Val Ser Asp Val Arg Ile Leu Gln Ser Tyr Tyr Asp Gln Gly  
590 595 600 605

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Asn Trp Cys Val Ile Leu Gln Lys Ala  
610

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caatattgca taatagtaac ccagttaact taccacttag gttagatttc ctggaggaac 3076  
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<212> PRT  
<213> Homo sapiens

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Glu Gly Ile Glu Thr Val Ser Tyr Ala Thr Gln Ser Leu Val Val Ala  
35 40 45  
Asn Gly Gly Leu Gly Asn Gly Val Ser Arg Asn Gln Leu Leu Pro Val  
50 55 60  
Leu Glu Lys Cys Gly Leu Val Asp Ala Leu Leu Met Pro Pro Asn Lys  
65 70 75 80  
Pro Tyr Ser Phe Ala Arg Tyr Arg Thr Thr Glu Glu Ser Lys Arg Ala  
85 90 95  
Tyr Val Thr Leu Asn Gly Lys Glu Val Val Asp Asp Leu Gly Gln Lys  
100 105 110  
Ile Thr Leu Tyr Leu Asn Phe Val Glu Lys Val Gln Trp Lys Glu Leu  
115 120 125

Arg Pro Gln Ala Leu Pro Pro Gly Leu Met Val Val Glu Glu Ile Ile  
130 135 140

Ser Ser Glu Glu Glu Lys Met Leu Leu Glu Ser Val Asp Trp Thr Glu  
145 150 155 160

Asp Thr Asp Asn Gln Asn Ser Gln Lys Ser Leu Lys His Arg Arg Val  
165 170 175

Lys His Phe Gly Tyr Glu Phe His Tyr Glu Asn Asn Asn Val Asp Lys  
180 185 190

Asp Lys Pro Leu Ser Gly Gly Leu Pro Asp Ile Cys Glu Ser Phe Leu  
195 200 205

Glu Lys Trp Leu Arg Lys Gly Tyr Ile Lys His Lys Pro Asp Gln Met  
210 215 220

Thr Ile Asn Gln Tyr Glu Pro Gly Gln Gly Ile Pro Ala His Ile Asp  
225 230 235 240

Thr His Ser Ala Phe Glu Asp Glu Ile Val Ser Leu Ser Leu Gly Ser  
245 250 255

Glu Ile Val Met Asp Phe Lys His Pro Asp Gly Ile Ala Val Pro Val  
260 265 270

Met Leu Pro Arg Arg Ser Leu Leu Val Met Thr Gly Glu Ser Arg Tyr  
275 280 285

Leu Trp Thr His Gly Ile Thr Cys Arg Lys Phe Asp Thr Val Gln Ala  
290 295 300

Ser Glu Ser Leu Lys Ser Gly Ile Ile Thr Ser Asp Val Gly Asp Leu  
305 310 315 320

Thr Leu Ser Lys Arg Gly Leu Arg Thr Ser Phe Thr Phe Arg Lys Val  
325 330 335

Arg Gln Thr Pro Cys Asn Cys Ser Tyr Pro Leu Val Cys Asp Ser Gln  
340 345 350

Arg Lys Glu Thr Pro Pro Ser Phe Pro Glu Ser Asp Lys Glu Ala Ser  
355 360 365

Arg Leu Glu Gln Glu Tyr Val His Gln Val Tyr Glu Glu Ile Ala Gly  
370 375 380

His Phe Ser Ser Thr Arg His Thr Pro Trp Pro His Ile Val Glu Phe  
385 390 395 400

Leu Lys Ala Leu Pro Ser Gly Ser Ile Val Ala Asp Ile Gly Cys Gly  
405 410 415

Asn Gly Lys Tyr Leu Gly Ile Asn Lys Glu Leu Tyr Met Glu Arg Arg  
420 425 430



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acg gct gac gcc aag ttt gag tca ggc gat gtg aag gcc aca gtg gca Thr Ala Asp Ala Lys Phe Glu Ser Gly Asp Val Lys Ala Thr Val Ala 55 60 65 70			245
gtg ctg agt ttc atc ctc tcc agt gcg gcc aag cac agt gtc gat ggc Val Leu Ser Phe Ile Leu Ser Ser Ala Ala Lys His Ser Val Asp Gly 75 80 85			293
gaa tcc ttg tcc agt gaa ctg cag cag ctg ggg ctg ccc aaa gag cac Glu Ser Leu Ser Ser Glu Leu Gln Gln Leu Gly Leu Pro Lys Glu His 90 95 100			341
gcg gcc agc ctg tgc cgc tgt tat gag gag aag caa agc ccc ttg cag Ala Ala Ser Leu Cys Arg Cys Tyr Glu Glu Lys Gln Ser Pro Leu Gln 105 110 115			389
aag cac ttg cgg gtc tgc agc cta cgc atg aat agg ttg gca ggt gtg Lys His Leu Arg Val Cys Ser Leu Arg Met Asn Arg Leu Ala Gly Val 120 125 130			437
ggc tgg cgg gtg gac tac acc ctg agc tcc agc ctg ctg caa tcc gtg Gly Trp Arg Val Asp Tyr Thr Leu Ser Ser Ser Leu Leu Gln Ser Val 135 140 145 150			485
gaa gag ccc atg gtg cac ctg cgg ctg gag gtg gca gct gcc cca ggg Glu Glu Pro Met Val His Leu Arg Leu Glu Val Ala Ala Ala Pro Gly 155 160 165			533
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gtc ctc ctg gca gaa ctg aag cag gcc cag acc ctg atg agc tcc ctg Val Leu Leu Ala Glu Leu Lys Gln Ala Gln Thr Leu Met Ser Ser Leu 185 190 195			629
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35 40 45

Glu Lys Ile Leu Lys Leu Thr Ala Asp Ala Lys Phe Glu Ser Gly Asp  
50 55 60

Val Lys Ala Thr Val Ala Val Leu Ser Phe Ile Leu Ser Ser Ala Ala  
65 70 75 80

Lys His Ser Val Asp Gly Glu Ser Leu Ser Ser Glu Leu Gln Gln Leu  
85 90 95

Gly Leu Pro Lys Glu His Ala Ala Ser Leu Cys Arg Cys Tyr Glu Glu  
100 105 110

Lys Gln Ser Pro Leu Gln Lys His Leu Arg Val Cys Ser Leu Arg Met  
115 120 125

Asn Arg Leu Ala Gly Val Gly Trp Arg Val Asp Tyr Thr Leu Ser Ser  
130 135 140

Ser Leu Leu Gln Ser Val Glu Glu Pro Met Val His Leu Arg Leu Glu  
145 150 155 160

Val Ala Ala Ala Pro Gly Thr Pro Ala Gln Pro Val Ala Met Ser Leu  
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Gly Asp Ser Gly Asn Leu Ile Ala Tyr Gly Gly Asn Asn Tyr Val Val	
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Ile Gly Thr Cys Thr Phe Gln Glu Glu Ala Asp Val Glu Gly Ile	
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cag tat aaa aca ctt cga aca ttt cac cat gga gtc agg gtt gat ggc	361
Gln Tyr Lys Thr Leu Arg Thr Phe His His Gly Val Arg Val Asp Gly	
65 70 75	
ata gct tgg agc cca gag act aga ctt gat tca ttg cct cca gta atc	409
Ile Ala Trp Ser Pro Glu Thr Arg Leu Asp Ser Leu Pro Pro Val Ile	
80 85 90	
aaa ttt tgt act tca gct gct gat atg aaa att aga tta ttt act tca	457
Lys Phe Cys Thr Ser Ala Ala Asp Met Lys Ile Arg Leu Phe Thr Ser	
95 100 105	
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Asp Leu Gln Asp Lys Asn Glu Tyr Lys Val Leu Glu Gly His Thr Asp	
110 115 120 125	
ttc att aat ggt ttg gtg ttt gat ccc aaa gaa ggc caa gaa att gca	553
Phe Ile Asn Gly Leu Val Phe Asp Pro Lys Glu Gly Gln Glu Ile Ala	
130 135 140	
agt gtg agt gac gat cac acc tgc agg att tgg aac ttg gaa gga gtg	601
Ser Val Ser Asp Asp His Thr Cys Arg Ile Trp Asn Leu Glu Gly Val	
145 150 155	
caa aca gct cat ttt gtt ctt cat tct cct ggc atg agt gtg tgc tgg	649
Gln Thr Ala His Phe Val Leu His Ser Pro Gly Met Ser Val Cys Trp	
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His Pro Glu Glu Thr Phe Lys Leu Met Val Ala Glu Lys Asn Gly Thr	
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Ile Arg Phe Tyr Asp Leu Leu Ala Gln Gln Ala Ile Leu Ser Leu Glu	
190 195 200 205	
tca gaa caa gtg cca tta atg tca gca cac tgg tgc tta aaa aac acc	793
Ser Glu Gln Val Pro Leu Met Ser Ala His Trp Cys Leu Lys Asn Thr	
210 215 220	
ttc aaa gtt gga gcc gtt gca gga aat gat tgg tta att tgg gat att	841

Phe Lys Val Gly Ala Val Ala Gly Asn Asp Trp Leu Ile Trp Asp Ile  
225 230 235

act cgg tcc agt tat cct caa aat aag aga cct gtt cac atg gat cga 889  
Thr Arg Ser Ser Tyr Pro Gln Asn Lys Arg Pro Val His Met Asp Arg  
240 245 250

gcc tgc tta ttc agg tgg tcc aca att agt gaa aat ctg ttt gca acc 937  
Ala Cys Leu Phe Arg Trp Ser Thr Ile Ser Glu Asn Leu Phe Ala Thr  
255 260 265

act ggt tat cct ggc aaa atg gca agc cag ttt caa att cat cat tta 985  
Thr Gly Tyr Pro Gly Lys Met Ala Ser Gln Phe Gln Ile His His Leu  
270 275 280 285

gga cac cct cag ccc atc ctc atg ggt tct gta gcc gtt gga tct gga 1033  
Gly His Pro Gln Pro Ile Leu Met Gly Ser Val Ala Val Gly Ser Gly  
290 295 300

ctg tcc tgg cat cga act ctc cct ctg tgt gta att gga gga gac cac 1081  
Leu Ser Trp His Arg Thr Leu Pro Leu Cys Val Ile Gly Gly Asp His  
305 310 315

aag ctg ttg ttt tgg gtg act gaa gta taa agtgttttct gtaccttaga 1131  
Lys Leu Leu Phe Trp Val Thr Glu Val  
320 325

ttcacaaact ttgtatTTTT agtacatatt ttgaagaatt tctatagtac atatTTTgaa 1191

gaatTTTTat atcaaatata ccgtatactt tagaaaatgt ctgagttgct tttattaaat 1251

aaaatggtga tggTTTgaaa aat 1274

<210> 22  
<211> 326  
<212> PRT  
<213> Homo sapiens

<400> 22  
Met Lys Gln Asp Ala Ser Arg Asn Ala Ala Tyr Thr Val Asp Cys Glu  
1 5 10 15

Asp Tyr Val His Val Val Glu Phe Asn Pro Phe Glu Asn Gly Asp Ser  
20 25 30

Gly Asn Leu Ile Ala Tyr Gly Gly Asn Asn Tyr Val Val Ile Gly Thr  
35 40 45

Cys Thr Phe Gln Glu Glu Glu Ala Asp Val Glu Gly Ile Gln Tyr Lys  
50 55 60

Thr Leu Arg Thr Phe His His Gly Val Arg Val Asp Gly Ile Ala Trp  
65 70 75 80

Ser Pro Glu Thr Arg Leu Asp Ser Leu Pro Pro Val Ile Lys Phe Cys  
85 90 95



cttttcgagg taggagtcga ctctgtgag gt atg gtg ctg ggt gca gat gca 53  
Met Val Leu Gly Ala Asp Ala  
1 5

gtg tgg ctc tgg ata gca cct tat gga cag ttg tgt ccc caa gga agg 101  
Val Trp Leu Trp Ile Ala Pro Tyr Gly Gln Leu Cys Pro Gln Gly Arg  
10 15 20

atg aga ata gct act gaa gtc cta aag agc aag cct aac tca agc cat 149  
Met Arg Ile Ala Thr Glu Val Leu Lys Ser Lys Pro Asn Ser Ser His  
25 30 35

tgg cac aca ggc att aga cag aaa gct gga agt tga aatgggtggag 195  
Trp His Thr Gly Ile Arg Gln Lys Ala Gly Ser  
40 45 50

tccaacttgc ctggaccagc ttaatgggtc tgctcctggt aacgttttta tccatggatg 255

acttgcttgg gtaaggacat gaagacagtt cctgtcatac cttttaaagg tacatgtttt 315

attgatgtta acgttaattg attgagctac tgtagtgat gatttttaaaa ttaaagcaga 375

tgggaatctc tctgagaaaag aaaatggaga ttaatcttaa actgaaacag tagttgggaa 435

atctttttaga aatccaccta ttactaccta ttggtaaagg agattaaatt tctacaggta 495

tggagagtcg gcttgactac actgtgtgga gcaagtttta aagaagcaaa ggactcagaa 555

ttcatgattg aagaaatgca ggcagacctg ttatcctaaa ctaggtgagt cagcttttgg 615

tacatgtgat gattttcagt gtaaccaatg atgtaatgat tctgccaaat gaaatataat 675

gatatcactg taaaaccgtt ccattttgat tctgaggtta ctctactaac aagcatcaca 735

catttgattt ttgccctgat taatatgttg gcttcgcttt cagggttttt aatgaccaca 795

acaagcaagc atgcagctta ctgcttgaaa gggctcttgcc tcacccaagc tagagtgcag 855

tggcctttga agcttactac agcctcaaac ttctgggctc aagtgatcct cagcctccca 915

tggtgtcttg tagactgcct gatggagtct catggcacia gaagattaaa acagtgtctc 975

caattttaat aaatttttgc aatcc 1000

<210> 24  
<211> 50  
<212> PRT  
<213> Homo sapiens

<400> 24  
Met Val Leu Gly Ala Asp Ala Val Trp Leu Trp Ile Ala Pro Tyr Gly  
1 5 10 15

Gln Leu Cys Pro Gln Gly Arg Met Arg Ile Ala Thr Glu Val Leu Lys  
20 25 30

Ser Lys Pro Asn Ser Ser His Trp His Thr Gly Ile Arg Gln Lys Ala  
 35 40 45

Gly Ser  
 50

<210> 25  
 <211> 1087  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (28)..(558)

<400> 25  
 agcttccggg tttcctgggc tactacg atg gcg atg agt ttc gag tgg ccg tgg 54  
 Met Ala Met Ser Phe Glu Trp Pro Trp  
 1 5

cag tat cgc ttc cca ccc ttc ttt acg tta caa ccg aat gtg gac act 102  
 Gln Tyr Arg Phe Pro Pro Phe Phe Thr Leu Gln Pro Asn Val Asp Thr  
 10 15 20 25

cgg cag aag cag ctg gcc gcc tgg tgc tcg ctg gtc ctg tcc ttc tgc 150  
 Arg Gln Lys Gln Leu Ala Ala Trp Cys Ser Leu Val Leu Ser Phe Cys  
 30 35 40

cgc ctg cac aaa cag tcc agc atg acg gtg atg gaa gct cag gag agc 198  
 Arg Leu His Lys Gln Ser Ser Met Thr Val Met Glu Ala Gln Glu Ser  
 45 50 55

ccg ctc ttc aac aac gtc aag cta cag cga aag ctt cct gtg gag tcg 246  
 Pro Leu Phe Asn Asn Val Lys Leu Gln Arg Lys Leu Pro Val Glu Ser  
 60 65 70

atc cag att gta tta gag gaa ctg agg aag aaa ggg aac ctc gag tgg 294  
 Ile Gln Ile Val Leu Glu Glu Leu Arg Lys Lys Gly Asn Leu Glu Trp  
 75 80 85

ttg gat aag agc aag tcc agc ttc ctg atc atg tgg cgg agg cca gaa 342  
 Leu Asp Lys Ser Lys Ser Ser Phe Leu Ile Met Trp Arg Arg Pro Glu  
 90 95 100 105

gaa tgg ggg aaa ctc atc tat cag tgg gtt tcc agg agt ggc cag aac 390  
 Glu Trp Gly Lys Leu Ile Tyr Gln Trp Val Ser Arg Ser Gly Gln Asn  
 110 115 120

aac tcc gtc ttt acc ctg tat gaa ctg act aat ggg gaa gac aca gag 438  
 Asn Ser Val Phe Thr Leu Tyr Glu Leu Thr Asn Gly Glu Asp Thr Glu  
 125 130 135

gat gag gag ttc cac ggg ctg gat gaa gcc act cta ctg cgg gct ctg 486  
 Asp Glu Glu Phe His Gly Leu Asp Glu Ala Thr Leu Leu Arg Ala Leu  
 140 145 150

09690633.092701

cag gcc cta cag cag gag cac aag gcc gag atc atc act gtc agc gat 534  
 Gln Ala Leu Gln Gln Glu His Lys Ala Glu Ile Ile Thr Val Ser Asp  
 155 160 165

ggc cga ggc gtc aag ttc ttc tag cagggacctg tctcccttta cttcttacct 588  
 Gly Arg Gly Val Lys Phe Phe  
 170 175

cccacctttc cagggctttc aaaaggagac agacccagtg tcccccaaag actggatctg 648  
 tgactccacc agactcaaaa ggactccagt cctgaaggct gggacctggg gatgggtttc 708  
 tcacacccca tatgtctgtc ccttggatag ggtgaggctg aagcaccagg gagaaaatat 768  
 gtgcttcttc tcgccctacc tcctttccca tcctagactg tccttgagcc aggggtctgta 828  
 aacctgacac tttatatgtg ttcacacatg taagtacata cacacatgcg cctgcagcac 888  
 atgcttctgt ctctctctcc tcccaccct ttagctgctg ttgcctccct tctcaggctg 948  
 gtgctggatc cttcctaggg gatgggggaa gccttgctg caggcagcct tccaggcaat 1008  
 atgaagatag gaggccacg ggcttgccag tgagaggtgt ggccccacac cgatttatga 1068  
 tattaaaatc tcaactccc 1087

<210> 26  
 <211> 176  
 <212> PRT  
 <213> Homo sapiens

<400> 26  
 Met Ala Met Ser Phe Glu Trp Pro Trp Gln Tyr Arg Phe Pro Pro Phe  
 1 5 10 15  
 Phe Thr Leu Gln Pro Asn Val Asp Thr Arg Gln Lys Gln Leu Ala Ala  
 20 25 30  
 Trp Cys Ser Leu Val Leu Ser Phe Cys Arg Leu His Lys Gln Ser Ser  
 35 40 45  
 Met Thr Val Met Glu Ala Gln Glu Ser Pro Leu Phe Asn Asn Val Lys  
 50 55 60  
 Leu Gln Arg Lys Leu Pro Val Glu Ser Ile Gln Ile Val Leu Glu Glu  
 65 70 75 80  
 Leu Arg Lys Lys Gly Asn Leu Glu Trp Leu Asp Lys Ser Lys Ser Ser  
 85 90 95  
 Phe Leu Ile Met Trp Arg Arg Pro Glu Glu Trp Gly Lys Leu Ile Tyr  
 100 105 110  
 Gln Trp Val Ser Arg Ser Gly Gln Asn Asn Ser Val Phe Thr Leu Tyr  
 115 120 125

TC220 00000000

Glu Leu Thr Asn Gly Glu Asp Thr Glu Asp Glu Glu Phe His Gly Leu  
 130 135 140

Asp Glu Ala Thr Leu Leu Arg Ala Leu Gln Ala Leu Gln Gln Glu His  
 145 150 155 160

Lys Ala Glu Ile Ile Thr Val Ser Asp Gly Arg Gly Val Lys Phe Phe  
 165 170 175

<210> 27  
 <211> 703  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (67)..(222)

<400> 27  
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gccgcg atg ttc cgg att gag ggc ctc gcg ccg aag ctg gac ccg gag 108  
 Met Phe Arg Ile Glu Gly Leu Ala Pro Lys Leu Asp Pro Glu  
 1 5 10

gag atg aaa cgg aag atg cgc gag gat gtg atc tcc tcc ata cgg aac 156  
 Glu Met Lys Arg Lys Met Arg Glu Asp Val Ile Ser Ser Ile Arg Asn  
 15 20 25 30

ttt ctc atc tac gtg gcc ctc ctg cga gtc act cca ttt atc tta aag 204  
 Phe Leu Ile Tyr Val Ala Leu Leu Arg Val Thr Pro Phe Ile Leu Lys  
 35 40 45

aaa ttg gac agc ata tga agacaggaca tcacatatga atgcacgata 252  
 Lys Leu Asp Ser Ile  
 50

tgaagagcct ggttacagtt tcgactcctc tctgcaagtg aataggccca gaaaggtgta 312

agagactcct tgaatggaca taaaattctg cttgttaaga acaagtttgg ctctggtaac 372

tgaccttcaa agctaaaata taaaactatt tgggaagtat gaaacgatgt ctcgtgatct 432

ggtgtaccct tatccctgtg acgtttggcc cctgacaata ctggtataat tgtaaataat 492

gtcaaactcc gttttctagc aagtattaag ggagctgtgt ctgaaatggc actgtcttgt 552

cagtcatttc tgtttacctt tttcttctgc ccagagtgtg tttgtgaaga gtctcttata 612

ttatgttttg tggaaatcag cacacaacca caatgacatt taagcacagg atcattatta 672

gtctatgttt ttaataaaca tatcaattaa g 703

<210> 28  
 <211> 51

<212> PRT  
 <213> Homo sapiens

<400> 28  
 Met Phe Arg Ile Glu Gly Leu Ala Pro Lys Leu Asp Pro Glu Glu Met  
     1                    5                    10                    15  
 Lys Arg Lys Met Arg Glu Asp Val Ile Ser Ser Ile Arg Asn Phe Leu  
           20                    25                    30  
 Ile Tyr Val Ala Leu Leu Arg Val Thr Pro Phe Ile Leu Lys Lys Leu  
           35                    40                    45  
 Asp Ser Ile  
           50

<210> 29  
 <211> 921  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (204)..(776)

<400> 29  
 ctcccccggc gcggtccgcc aggccagtgc cctcagcatc tccaccccga ggtgggtttga 60  
 actttgagcc ttttgtagtc ctgatgaata atttcatttt cctcaagttt atgacactcg 120  
 gaacgtcaag aactggaggt ttgtgcaatt tgagaccggt cggcactgtg cagagatcag 180  
 agtactaaga gacagagatt aaa atg gct tcc aga gga aag aca gag aca agc 233  
                     Met Ala Ser Arg Gly Lys Thr Glu Thr Ser  
                                 1                    5                    10  
 aaa tta aag cag aat tta gaa gaa cag ttg gat aga ctc atg caa caa 281  
 Lys Leu Lys Gln Asn Leu Glu Glu Gln Leu Asp Arg Leu Met Gln Gln  
                     15                    20                    25  
 tta caa gat ctg gag gaa tgc aga gag gaa ctt gat aca gat gaa tat 329  
 Leu Gln Asp Leu Glu Glu Cys Arg Glu Glu Leu Asp Thr Asp Glu Tyr  
                     30                    35                    40  
 gaa gaa acc aaa aag gaa act ctg gag caa cta agt gaa ttt aat gat 377  
 Glu Glu Thr Lys Lys Glu Thr Leu Glu Gln Leu Ser Glu Phe Asn Asp  
                     45                    50                    55  
 tca cta aag aaa att atg tct gga aat atg act ttg gta gat gaa cta 425  
 Ser Leu Lys Lys Ile Met Ser Gly Asn Met Thr Leu Val Asp Glu Leu  
                     60                    65                    70  
 agt gga atg cag ctg gct att cag gca gct atc agc cag gcc ttt aaa 473  
 Ser Gly Met Gln Leu Ala Ile Gln Ala Ala Ile Ser Gln Ala Phe Lys  
                     75                    80                    85                    90

acc cca gag gtc atc aga ttg ttt gca aag aaa caa cca ggt cag ctt 521  
 Thr Pro Glu Val Ile Arg Leu Phe Ala Lys Lys Gln Pro Gly Gln Leu  
                   95                  100                  105

cgg aca agg tta gca gag atg gat aga gat ctg atg gta gga aag ctg 569  
 Arg Thr Arg Leu Ala Glu Met Asp Arg Asp Leu Met Val Gly Lys Leu  
                   110                  115                  120

gaa aga gac ctg tac act caa cag aaa gtg gag ata cta aca gct ctt 617  
 Glu Arg Asp Leu Tyr Thr Gln Gln Lys Val Glu Ile Leu Thr Ala Leu  
                   125                  130                  135

agg aaa ctt gga gag aag ctg act gca gat gat gag gcc ttc ttg tca 665  
 Arg Lys Leu Gly Glu Lys Leu Thr Ala Asp Asp Glu Ala Phe Leu Ser  
                   140                  145                  150

gca aat gca ggt gct ata ctc agc cag ttt gag aaa gtc tct aca gac 713  
 Ala Asn Ala Gly Ala Ile Leu Ser Gln Phe Glu Lys Val Ser Thr Asp  
                   155                  160                  165                  170

ctt ggc tct gga gac aaa att ctt gct ctg gca agt ttt gag gtt gaa 761  
 Leu Gly Ser Gly Asp Lys Ile Leu Ala Leu Ala Ser Phe Glu Val Glu  
                   175                  180                  185

aaa aca aaa aaa tga catggtgcag aagcttgtaa cattgatcac attcctaatg 816  
 Lys Thr Lys Lys  
                   190

taaatggtgt ctttcttctg gggttttcag ttattgcaaaa gaaatgaaga gattctggaa 876

atgcatcaat aacctaagaa aaagcgacat aaaaatatac ttatg 921

<210> 30  
 <211> 190  
 <212> PRT  
 <213> Homo sapiens

<400> 30  
 Met Ala Ser Arg Gly Lys Thr Glu Thr Ser Lys Leu Lys Gln Asn Leu  
   1                  5                  10                  15

Glu Glu Gln Leu Asp Arg Leu Met Gln Gln Leu Gln Asp Leu Glu Glu  
                   20                  25                  30

Cys Arg Glu Glu Leu Asp Thr Asp Glu Tyr Glu Glu Thr Lys Lys Glu  
                   35                  40                  45

Thr Leu Glu Gln Leu Ser Glu Phe Asn Asp Ser Leu Lys Lys Ile Met  
                   50                  55                  60

Ser Gly Asn Met Thr Leu Val Asp Glu Leu Ser Gly Met Gln Leu Ala  
                   65                  70                  75                  80

Ile Gln Ala Ala Ile Ser Gln Ala Phe Lys Thr Pro Glu Val Ile Arg  
                   85                  90                  95

Leu Phe Ala Lys Lys Gln Pro Gly Gln Leu Arg Thr Arg Leu Ala Glu  
100 105 110

Met Asp Arg Asp Leu Met Val Gly Lys Leu Glu Arg Asp Leu Tyr Thr  
115 120 125

Gln Gln Lys Val Glu Ile Leu Thr Ala Leu Arg Lys Leu Gly Glu Lys  
130 135 140

Leu Thr Ala Asp Asp Glu Ala Phe Leu Ser Ala Asn Ala Gly Ala Ile  
145 150 155 160

Leu Ser Gln Phe Glu Lys Val Ser Thr Asp Leu Gly Ser Gly Asp Lys  
165 170 175

Ile Leu Ala Leu Ala Ser Phe Glu Val Glu Lys Thr Lys Lys  
180 185 190

<210> 31  
<211> 584  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (41)..(418)

<400> 31  
ttttttccgg ttccggcctg gcgagagttt gtgcggcgac atg aaa ctg ctt acc 55  
Met Lys Leu Leu Thr  
1 5

cac aat ctg ctg agc tcg cat gtg cgg ggg gtg ggg tcc cgt ggc ttc 103  
His Asn Leu Leu Ser Ser His Val Arg Gly Val Gly Ser Arg Gly Phe  
10 15 20

ccc ctg cgc ctc cag gcc acc gag gtc cgt atc tgc cct gtg gaa ttc 151  
Pro Leu Arg Leu Gln Ala Thr Glu Val Arg Ile Cys Pro Val Glu Phe  
25 30 35

aac ccc aac ttc gtg gcg cgt atg ata cct aaa gtg gag tgg tcg gcg 199  
Asn Pro Asn Phe Val Ala Arg Met Ile Pro Lys Val Glu Trp Ser Ala  
40 45 50

ttc ctg gag gcg gcc gat aac ttg cgt ctg atc cag gtg ccg aaa ggg 247  
Phe Leu Glu Ala Ala Asp Asn Leu Arg Leu Ile Gln Val Pro Lys Gly  
55 60 65

ccg gtt gag gga tat gag gag aat gag gag ttt ctg agg acc atg cac 295  
Pro Val Glu Gly Tyr Glu Glu Asn Glu Glu Phe Leu Arg Thr Met His  
70 75 80 85

cac ctg ctg ctg gag gtg gaa gtg ata gag ggc acc ctg cag tgc ccg 343  
His Leu Leu Leu Glu Val Glu Val Ile Glu Gly Thr Leu Gln Cys Pro  
90 95 100

gaa tct gga cgt atg ttc ccc atc agc cgc ggg atc ccc aac atg ctg 391  
 Glu Ser Gly Arg Met Phe Pro Ile Ser Arg Gly Ile Pro Asn Met Leu  
                   105                  110                  115

ctg agt gaa gag gaa act gag agt tga ttgtgccagg cgccagtttt 438  
 Leu Ser Glu Glu Glu Thr Glu Ser  
                   120                  125

tcttggttatg actgtgtatt tttgttgatc tataccctgt ttccgaattc tgccgtgtgt 498

atccccaacc cttgacccaa tgacaccaa cacagtgttt ttgagctcgg tattatatat 558

ttttttctca tttaaagttt aaaacc 584

<210> 32  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 32  
 Met Lys Leu Leu Thr His Asn Leu Leu Ser Ser His Val Arg Gly Val  
   1                  5                  10                  15  
 Gly Ser Arg Gly Phe Pro Leu Arg Leu Gln Ala Thr Glu Val Arg Ile  
                   20                  25                  30  
 Cys Pro Val Glu Phe Asn Pro Asn Phe Val Ala Arg Met Ile Pro Lys  
                   35                  40                  45  
 Val Glu Trp Ser Ala Phe Leu Glu Ala Ala Asp Asn Leu Arg Leu Ile  
                   50                  55                  60  
 Gln Val Pro Lys Gly Pro Val Glu Gly Tyr Glu Glu Asn Glu Glu Phe  
                   65                  70                  75                  80  
 Leu Arg Thr Met His His Leu Leu Leu Glu Val Glu Val Ile Glu Gly  
                   85                  90                  95  
 Thr Leu Gln Cys Pro Glu Ser Gly Arg Met Phe Pro Ile Ser Arg Gly  
                   100                  105                  110  
 Ile Pro Asn Met Leu Leu Ser Glu Glu Glu Thr Glu Ser  
                   115                  120                  125

<210> 33  
 <211> 875  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (25)..(555)

<400> 33  
 ctttgcgagg cacctggcga caaa atg gct gcc cga ggg aga cgg gcg gag 51

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Met Ala Ala Arg Gly Arg Arg Ala Glu  
1 5

cct cag ggc cgg gag gct ccg ggc ccc gcg ggc ggt ggc ggt ggc ggg	99
Pro Gln Gly Arg Glu Ala Pro Gly Pro Ala Gly Gly Gly Gly Gly Gly	
10 15 20 25	
agc cgt tgg gct gag tcg gga tcg ggg acg tcg ccc gag agc ggg gac	147
Ser Arg Trp Ala Glu Ser Gly Ser Gly Thr Ser Pro Glu Ser Gly Asp	
30 35 40	
gag gag gtg tcg ggc gcg ggt tcg agc ccg gtg tcg ggc ggc gtg aac	195
Glu Glu Val Ser Gly Ala Gly Ser Ser Pro Val Ser Gly Gly Val Asn	
45 50 55	
ttg ttc gcc aac gac ggc agc ttc ctg gag ctg ttc aag cgg aag atg	243
Leu Phe Ala Asn Asp Gly Ser Phe Leu Glu Leu Phe Lys Arg Lys Met	
60 65 70	
gag gag gag cag cgg cag cgg cag gag gag ccg ccc ccg ggt ccg cag	291
Glu Glu Glu Gln Arg Gln Arg Gln Glu Glu Pro Pro Pro Gly Pro Gln	
75 80 85	
cga ccc gac cag tcg gcc gcc gcc gct ggc ccc ggg gat ccg aag agg	339
Arg Pro Asp Gln Ser Ala Ala Ala Ala Gly Pro Gly Asp Pro Lys Arg	
90 95 100 105	
aag ggc ggt ccg ggc tcc aca ctt agc ttc gtg ggc aaa cgc aga ggc	387
Lys Gly Gly Pro Gly Ser Thr Leu Ser Phe Val Gly Lys Arg Arg Gly	
110 115 120	
ggg aac aaa cta gcc ctc aag acg gga ata gta gcc aag aag cag aag	435
Gly Asn Lys Leu Ala Leu Lys Thr Gly Ile Val Ala Lys Lys Gln Lys	
125 130 135	
acg gag gat gag gta tta aca agt aaa ggt gac gcg tgg gcc aag tac	483
Thr Glu Asp Glu Val Leu Thr Ser Lys Gly Asp Ala Trp Ala Lys Tyr	
140 145 150	
atg gca gaa gtg aaa aag tac aaa gct cac cag tgc ggt gac gat gat	531
Met Ala Glu Val Lys Lys Tyr Lys Ala His Gln Cys Gly Asp Asp Asp	
155 160 165	
aaa act cgg ccc ctg gtg aaa tga cgccccctccc ccacctgccc atggcctggg	585
Lys Thr Arg Pro Leu Val Lys	
170 175	
actctctgcg atgtacataa ctattttaatg cagcggcagc ggcgacagcc ttccctgaga	645
ggacttaaaa gcagaaggaa accgagatgc ttcccgagc cgtggacgat tctccaggac	705
tcttttttta ccttgagcac ttgcctcgtg agacttcata gaacagtggg ttactgtccc	765
cccccttctca cctctctatt ctctctggct ctttctgtct tctctttctc accctcctcc	825
ctcccccttag ccatcacttc tgggaagtaa agaacttgac ttagtgccgg	875

<210> 34  
 <211> 176  
 <212> PRT  
 <213> Homo sapiens

<400> 34  
 Met Ala Ala Arg Gly Arg Arg Ala Glu Pro Gln Gly Arg Glu Ala Pro  
           1                  5                  10                  15  
 Gly Pro Ala Gly Gly Gly Gly Gly Gly Ser Arg Trp Ala Glu Ser Gly  
                   20                  25                  30  
 Ser Gly Thr Ser Pro Glu Ser Gly Asp Glu Glu Val Ser Gly Ala Gly  
           35                  40                  45  
 Ser Ser Pro Val Ser Gly Gly Val Asn Leu Phe Ala Asn Asp Gly Ser  
           50                  55                  60  
 Phe Leu Glu Leu Phe Lys Arg Lys Met Glu Glu Glu Gln Arg Gln Arg  
           65                  70                  75                  80  
 Gln Glu Glu Pro Pro Pro Gly Pro Gln Arg Pro Asp Gln Ser Ala Ala  
                   85                  90                  95  
 Ala Ala Gly Pro Gly Asp Pro Lys Arg Lys Gly Gly Pro Gly Ser Thr  
           100                  105                  110  
 Leu Ser Phe Val Gly Lys Arg Arg Gly Gly Asn Lys Leu Ala Leu Lys  
           115                  120                  125  
 Thr Gly Ile Val Ala Lys Lys Gln Lys Thr Glu Asp Glu Val Leu Thr  
           130                  135                  140  
 Ser Lys Gly Asp Ala Trp Ala Lys Tyr Met Ala Glu Val Lys Lys Tyr  
           145                  150                  155                  160  
 Lys Ala His Gln Cys Gly Asp Asp Asp Lys Thr Arg Pro Leu Val Lys  
                   165                  170                  175

<210> 35  
 <211> 470  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (216)..(374)

<400> 35  
 ctttagtcgtg tgtacatcat tgggaatgga gggaaataaa tgactggatg gtcgctgctt 60  
 tttaagtttc aaattgacat tccagacaag cggtgcctga gcccgtcctt gtcttcagat 120  
 cttcacagca cagttcctgg gaaggtggag ccaccagcct ctcttgaat aactgggaga 180

tgaacagga agctctatga cacacttgat cgaat atg aca gac acc gaa aat 233  
Met Thr Asp Thr Glu Asn  
1 5

cac gac tca gcc ccc tcc agc acc tct acc tgt tgc ccg ccg atc aca 281  
His Asp Ser Ala Pro Ser Ser Thr Ser Thr Cys Cys Pro Pro Ile Thr  
10 15 20

gcc gga atg cag ctg aaa gat tcc ctg ggg cct ggt tcc aac cgc cca 329  
Ala Gly Met Gln Leu Lys Asp Ser Leu Gly Pro Gly Ser Asn Arg Pro  
25 30 35

ctg tgg act ctg agg cct ctg cat ttg tgg gtg gtc tgc ctg tga 374  
Leu Trp Thr Leu Arg Pro Leu His Leu Trp Val Val Cys Leu  
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ttaatccctt gtccttcatt aaaagcaaaa ctaaag 470

<210> 36  
<211> 52  
<212> PRT  
<213> Homo sapiens

<400> 36  
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Val Val Cys Leu  
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<210> 37  
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<212> DNA  
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<220>  
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<400> 37  
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Met Lys Leu Lys Asp Thr Lys Ser Arg Pro Lys Gln Ser  
1 5 10

agc tgt ggc aaa ttt cag aca aag gga atc aaa gtt gtg gga aaa tgg 159



240	245	250	
gcg gtg ttg cag tgg cag aag agg aat gct gcc cct cct cca agt aac Ala Val Leu Gln Trp Gln Lys Arg Asn Ala Ala Pro Pro Pro Ser Asn 255 260 265			879
acc gaa gca cca cct gga gag acc aga act gag gcc gga gct gag act Thr Glu Ala Pro Pro Gly Glu Thr Arg Thr Glu Ala Gly Ala Glu Thr 270 275 280 285			927
aga tca cca ggc aag gct gaa gct gag tct gat gca ttg cct gac gat Arg Ser Pro Gly Lys Ala Glu Ala Glu Ser Asp Ala Leu Pro Asp Asp 290 295 300			975
act gta att gag agt gaa gca ctg ccc agt gat att gca gcc gag gcc Thr Val Ile Glu Ser Glu Ala Leu Pro Ser Asp Ile Ala Ala Glu Ala 305 310 315			1023
aga gcc aag act gga ggc act gtc tca gac cag gcg ttg ctc ttt ggt Arg Ala Lys Thr Gly Gly Thr Val Ser Asp Gln Ala Leu Leu Phe Gly 320 325 330			1071
gac gat gat gct ggt gaa ggg cct tct tcc ctg atc agg gag aaa cct Asp Asp Asp Ala Gly Glu Gly Pro Ser Ser Leu Ile Arg Glu Lys Pro 335 340 345			1119
gtt ccc aaa cag aat gag aat gag gag gaa aat ctt gat aaa gag cag Val Pro Lys Gln Asn Glu Asn Glu Glu Glu Asn Leu Asp Lys Glu Gln 350 355 360 365			1167
act gga aat cta aaa cag gag ttg gat gac aaa agc gcc acc tgt aag Thr Gly Asn Leu Lys Gln Glu Leu Asp Asp Lys Ser Ala Thr Cys Lys 370 375 380			1215
gca tat cca aag cgt cct ctg ctt gga ctg gtt ctg act ccc act cga Ala Tyr Pro Lys Arg Pro Leu Leu Gly Leu Val Leu Thr Pro Thr Arg 385 390 395			1263
gag ctg gcc gtc cag gtc aaa cag cac att gat gct gtg gcc agg ttt Glu Leu Ala Val Gln Val Lys Gln His Ile Asp Ala Val Ala Arg Phe 400 405 410			1311
aca gga att aaa act gct att ttg gtt ggt gga atg tcc acg cag aaa Thr Gly Ile Lys Thr Ala Ile Leu Val Gly Gly Met Ser Thr Gln Lys 415 420 425			1359
cag cag agg atg ctg aac cgt cgt cct gag att gtg gtt gct act cca Gln Gln Arg Met Leu Asn Arg Arg Pro Glu Ile Val Val Ala Thr Pro 430 435 440 445			1407
ggc cgg ctg tgg gaa tta att aaa gaa aag cat tat cat ttg agg aac Gly Arg Leu Trp Glu Leu Ile Lys Glu Lys His Tyr His Leu Arg Asn 450 455 460			1455
ctt cgg cag ctc agg tgc ctg gta gtg gat gag gct gac cgg atg gtt Leu Arg Gln Leu Arg Cys Leu Val Val Asp Glu Ala Asp Arg Met Val 465 470 475			1503

gag aaa ggc cat ttt gct gag ctc tca cag ctg cta gag atg ctc aat	1551
Glu Lys Gly His Phe Ala Glu Leu Ser Gln Leu Leu Glu Met Leu Asn	
480 485 490	
gac tcc caa tac aac cca aag aga caa acg ctt gtt ttt tct gcc aca	1599
Asp Ser Gln Tyr Asn Pro Lys Arg Gln Thr Leu Val Phe Ser Ala Thr	
495 500 505	
ctc acc ctg gtg cat cag gct cct gct cga atc ctt cat aag aag cac	1647
Leu Thr Leu Val His Gln Ala Pro Ala Arg Ile Leu His Lys Lys His	
510 515 520 525	
acc aag aaa atg gat aaa aca gcc aaa ctt gac ctc ctt atg cag aaa	1695
Thr Lys Lys Met Asp Lys Thr Ala Lys Leu Asp Leu Leu Met Gln Lys	
530 535 540	
att ggc atg agg ggc aag ccc aag gtc att gac ctc aca agg aat gag	1743
Ile Gly Met Arg Gly Lys Pro Lys Val Ile Asp Leu Thr Arg Asn Glu	
545 550 555	
gcc acg gtg gag acg cta aca gag acc aag atc cat tgt gag act gat	1791
Ala Thr Val Glu Thr Leu Thr Glu Thr Lys Ile His Cys Glu Thr Asp	
560 565 570	
gag aaa gac ttc tac ttg tac tac ttc ctg atg cag tat cca ggc cgc	1839
Glu Lys Asp Phe Tyr Leu Tyr Tyr Phe Leu Met Gln Tyr Pro Gly Arg	
575 580 585	
agc tta gtg ttt gcc aac agt atc tcc tgc atc aaa cgc ctc tct ggg	1887
Ser Leu Val Phe Ala Asn Ser Ile Ser Cys Ile Lys Arg Leu Ser Gly	
590 595 600 605	
ctc ctc aaa gtc ctt gat atc atg ccc ttg acc ctg cat gcc tgt atg	1935
Leu Leu Lys Val Leu Asp Ile Met Pro Leu Thr Leu His Ala Cys Met	
610 615 620	
cac cag aag cag agg ctc aga aac ctg gag cag ttt gcc cgt ctg gaa	1983
His Gln Lys Gln Arg Leu Arg Asn Leu Glu Gln Phe Ala Arg Leu Glu	
625 630 635	
gac tgt gtt ctc ttg gca aca gat gtg gca gct cgg ggt ctg gat att	2031
Asp Cys Val Leu Leu Ala Thr Asp Val Ala Ala Arg Gly Leu Asp Ile	
640 645 650	
cct aaa gtc cag cat gtc atc cat tac cag gtc cca cgt acc tcg gag	2079
Pro Lys Val Gln His Val Ile His Tyr Gln Val Pro Arg Thr Ser Glu	
655 660 665	
att tat gtc cac cga agt ggt cga act gct cga gct acc aat gaa ggc	2127
Ile Tyr Val His Arg Ser Gly Arg Thr Ala Arg Ala Thr Asn Glu Gly	
670 675 680 685	
ctc agt ctg atg ctc att ggg cct gag gat gtg atc aac ttt aag aag	2175
Leu Ser Leu Met Leu Ile Gly Pro Glu Asp Val Ile Asn Phe Lys Lys	
690 695 700	

att tac aaa acg ctc aag aaa gat gag gat atc cca ctg ttc ccc gtg 2223  
 ile Tyr Lys Thr Leu Lys Lys Asp Glu Asp Ile Pro Leu Phe Pro Val  
 705 710 715

cag aca aaa tac atg gat gtg gtc aag gag cga atc cgt tta gct cga 2271  
 Gln Thr Lys Tyr Met Asp Val Val Lys Glu Arg Ile Arg Leu Ala Arg  
 720 725 730

cag att gag aaa tct gag tat cgg aac ttc cag gct tgc ctg cac aac 2319  
 Gln Ile Glu Lys Ser Glu Tyr Arg Asn Phe Gln Ala Cys Leu His Asn  
 735 740 745

tct tgg att gag cag gca gca gct gcc ctg gag att gag ctg gaa gaa 2367  
 Ser Trp Ile Glu Gln Ala Ala Ala Ala Leu Glu Ile Glu Leu Glu Glu  
 750 755 760 765

gac atg tat aag gga gga aaa gct gac cag caa gaa gaa cgt cgg aga 2415  
 Asp Met Tyr Lys Gly Gly Lys Ala Asp Gln Gln Glu Glu Arg Arg Arg  
 770 775 780

caa aag cag atg aag gtt ctg aag aag gag ctg cgc cac ctg ctg tcc 2463  
 Gln Lys Gln Met Lys Val Leu Lys Lys Glu Leu Arg His Leu Leu Ser  
 785 790 795

cag cca ctg ttt acg gag agc cag aaa acc aag tat ccc act cag tct 2511  
 Gln Pro Leu Phe Thr Glu Ser Gln Lys Thr Lys Tyr Pro Thr Gln Ser  
 800 805 810

ggc aag ccg ccc ctg ctt gtg tct gcc cca agt aag agc gag tct gct 2559  
 Gly Lys Pro Pro Leu Leu Val Ser Ala Pro Ser Lys Ser Glu Ser Ala  
 815 820 825

ttg agc tgt ctc tcc aag cag aag aag aag aag aca aag aag ccg aag 2607  
 Leu Ser Cys Leu Ser Lys Gln Lys Lys Lys Lys Thr Lys Lys Pro Lys  
 830 835 840 845

gag cca cag ccg gaa cag cca cag cca agt aca agt gca aat taa 2652  
 Glu Pro Gln Pro Glu Gln Pro Gln Pro Ser Thr Ser Ala Asn  
 850 855

ctgggtcaagt gtgtcagtga ctgcacattg gtttctgttc tctggctatt tgcaaaacct 2712

ctccccacct tgtgttttcac tccaccacca accccaggta aaaaagtctc cctctcttcc 2772

actcacacccc atagcgggag agacctcatg cagatttgca ttgttttgga gtaagaattc 2832

aatgcagcag cttaattttt ctgtattgca gtgttttatag gcttcttgtg tgttaaactt 2892

gatttcataa attaaaaaca atggtcag 2920

<210> 38  
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 <212> PRT  
 <213> Homo sapiens

<400> 38  
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Lys	Ile	Asp	Pro	Asn	Met	Phe	Ala	Asp	Gly	Gln	Met	Asp	Asp	Leu	Val
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Cys	Phe	Glu	Glu	Leu	Thr	Asp	Tyr	Gln	Leu	Val	Ser	Pro	Ala	Lys	Asn
	50					55					60				
Pro	Ser	Ser	Leu	Phe	Ser	Lys	Glu	Ala	Pro	Lys	Arg	Lys	Ala	Gln	Ala
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Val	Ser	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	Lys	Ser	Ser	Ser	Pro	Lys
			85					90						95	
Lys	Lys	Ile	Lys	Leu	Lys	Lys	Ser	Lys	Asn	Val	Ala	Thr	Glu	Gly	Thr
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Ser	Thr	Gln	Lys	Glu	Phe	Glu	Val	Lys	Asp	Pro	Glu	Leu	Glu	Ala	Gln
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Gly	Asp	Asp	Met	Val	Cys	Asp	Asp	Pro	Glu	Ala	Gly	Glu	Met	Thr	Ser
	130					135					140				
Glu	Asn	Leu	Val	Gln	Thr	Ala	Pro	Lys	Lys	Lys	Asn	Lys	Gly	Lys	
	145				150				155					160	
Lys	Gly	Leu	Glu	Pro	Ser	Gln	Ser	Thr	Ala	Ala	Lys	Val	Pro	Lys	Lys
			165					170						175	
Ala	Lys	Thr	Trp	Ile	Pro	Glu	Val	His	Asp	Gln	Lys	Ala	Asp	Val	Ser
			180					185					190		
Ala	Trp	Lys	Asp	Leu	Phe	Val	Pro	Arg	Pro	Val	Leu	Arg	Ala	Leu	Ser
		195					200					205			
Phe	Leu	Gly	Phe	Ser	Ala	Pro	Thr	Pro	Ile	Gln	Ala	Leu	Thr	Leu	Ala
	210					215				220					
Pro	Ala	Ile	Arg	Asp	Lys	Leu	Asp	Ile	Leu	Gly	Ala	Ala	Glu	Thr	Gly
	225			230					235					240	
Ser	Gly	Lys	Thr	Leu	Ala	Phe	Ala	Ile	Pro	Met	Ile	His	Ala	Val	Leu
			245					250						255	
Gln	Trp	Gln	Lys	Arg	Asn	Ala	Ala	Pro	Pro	Pro	Ser	Asn	Thr	Glu	Ala
		260						265					270		
Pro	Pro	Gly	Glu	Thr	Arg	Thr	Glu	Ala	Gly	Ala	Glu	Thr	Arg	Ser	Pro
		275					280					285			
Gly	Lys	Ala	Glu	Ala	Glu	Ser	Asp	Ala	Leu	Pro	Asp	Asp	Thr	Val	Ile
	290					295					300				
Glu	Ser	Glu	Ala	Leu	Pro	Ser	Asp	Ile	Ala	Ala	Glu	Ala	Arg	Ala	Lys
	305				310				315					320	
Thr	Gly	Gly	Thr	Val	Ser	Asp	Gln	Ala	Leu	Leu	Phe	Gly	Asp	Asp	Asp
			325					330						335	
Ala	Gly	Glu	Gly	Pro	Ser	Ser	Leu	Ile	Arg	Glu	Lys	Pro	Val	Pro	Lys
			340					345					350		
Gln	Asn	Glu	Asn	Glu	Glu	Glu	Asn	Leu	Asp	Lys	Glu	Gln	Thr	Gly	Asn
	355						360					365			
Leu	Lys	Gln	Glu	Leu	Asp	Asp	Lys	Ser	Ala	Thr	Cys	Lys	Ala	Tyr	Pro
	370				375						380				
Lys	Arg	Pro	Leu	Leu	Gly	Leu	Val	Leu	Thr	Pro	Thr	Arg	Glu	Leu	Ala
	385				390					395				400	
Val	Gln	Val	Lys	Gln	His	Ile	Asp	Ala	Val	Ala	Arg	Phe	Thr	Gly	Ile
			405					410						415	
Lys	Thr	Ala	Ile	Leu	Val	Gly	Gly	Met	Ser	Thr	Gln	Lys	Gln	Gln	Arg
			420				425						430		
Met	Leu	Asn	Arg	Arg	Pro	Glu	Ile	Val	Val	Ala	Thr	Pro	Gly	Arg	Leu
		435				440						445			
Trp	Glu	Leu	Ile	Lys	Glu	Lys	His	Tyr	His	Leu	Arg	Asn	Leu	Arg	Gln
	450					455					460				

Leu Arg Cys Leu Val Val Asp Glu Ala Asp Arg Met Val Glu Lys Gly  
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 His Phe Ala Glu Leu Ser Gln Leu Leu Glu Met Leu Asn Asp Ser Gln  
 485 490 495  
 Tyr Asn Pro Lys Arg Gln Thr Leu Val Phe Ser Ala Thr Leu Thr Leu  
 500 505 510  
 Val His Gln Ala Pro Ala Arg Ile Leu His Lys Lys His Thr Lys Lys  
 515 520 525  
 Met Asp Lys Thr Ala Lys Leu Asp Leu Leu Met Gln Lys Ile Gly Met  
 530 535 540  
 Arg Gly Lys Pro Lys Val Ile Asp Leu Thr Arg Asn Glu Ala Thr Val  
 545 550 555 560  
 Glu Thr Leu Thr Glu Thr Lys Ile His Cys Glu Thr Asp Glu Lys Asp  
 565 570 575  
 Phe Tyr Leu Tyr Tyr Phe Leu Met Gln Tyr Pro Gly Arg Ser Leu Val  
 580 585 590  
 Phe Ala Asn Ser Ile Ser Cys Ile Lys Arg Leu Ser Gly Leu Leu Lys  
 595 600 605  
 Val Leu Asp Ile Met Pro Leu Thr Leu His Ala Cys Met His Gln Lys  
 610 615 620  
 Gln Arg Leu Arg Asn Leu Glu Gln Phe Ala Arg Leu Glu Asp Cys Val  
 625 630 635 640  
 Leu Leu Ala Thr Asp Val Ala Ala Arg Gly Leu Asp Ile Pro Lys Val  
 645 650 655  
 Gln His Val Ile His Tyr Gln Val Pro Arg Thr Ser Glu Ile Tyr Val  
 660 665 670  
 His Arg Ser Gly Arg Thr Ala Arg Ala Thr Asn Glu Gly Leu Ser Leu  
 675 680 685  
 Met Leu Ile Gly Pro Glu Asp Val Ile Asn Phe Lys Lys Ile Tyr Lys  
 690 695 700  
 Thr Leu Lys Lys Asp Glu Asp Ile Pro Leu Phe Pro Val Gln Thr Lys  
 705 710 715 720  
 Tyr Met Asp Val Val Lys Glu Arg Ile Arg Leu Ala Arg Gln Ile Glu  
 725 730 735  
 Lys Ser Glu Tyr Arg Asn Phe Gln Ala Cys Leu His Asn Ser Trp Ile  
 740 745 750  
 Glu Gln Ala Ala Ala Ala Leu Glu Ile Glu Leu Glu Glu Asp Met Tyr  
 755 760 765  
 Lys Gly Gly Lys Ala Asp Gln Gln Glu Glu Arg Arg Arg Gln Lys Gln  
 770 775 780  
 Met Lys Val Leu Lys Lys Glu Leu Arg His Leu Leu Ser Gln Pro Leu  
 785 790 795 800  
 Phe Thr Glu Ser Gln Lys Thr Lys Tyr Pro Thr Gln Ser Gly Lys Pro  
 805 810 815  
 Pro Leu Leu Val Ser Ala Pro Ser Lys Ser Glu Ser Ala Leu Ser Cys  
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<210> 39  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (15)..(998)

<400> 39

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Cys Gly Arg Gly Trp Ser Arg Ala Met Arg Gly Cys Gln Leu Leu Gly	
15 20 25	
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Leu Arg Ser Ser Trp Pro Gly Asp Leu Leu Ser Ala Arg Leu Leu Ser	
30 35 40	
caa gag aag cgg gca gcg gaa acg cac ttt ggg ttt gag act gtg tcg	194
Gln Glu Lys Arg Ala Ala Glu Thr His Phe Gly Phe Glu Thr Val Ser	
45 50 55 60	
gaa gag gag aag ggg ggc aaa gtc tat cag gtg ttt gaa agt gtg gct	242
Glu Glu Glu Lys Gly Gly Lys Val Tyr Gln Val Phe Glu Ser Val Ala	
65 70 75	
aag aag tat gat gtg atg aat gat atg atg agt ctt ggt atc cat cgt	290
Lys Lys Tyr Asp Val Met Asn Asp Met Met Ser Leu Gly Ile His Arg	
80 85 90	
gtt tgg aag gat ttg ctg ctc tgg aag atg cac ccg ctt cct ggg acc	338
Val Trp Lys Asp Leu Leu Leu Trp Lys Met His Pro Leu Pro Gly Thr	
95 100 105	
cag ctg ctt gat gtt gct gga ggc aca ggt gac att gca ttc cgg ttc	386
Gln Leu Leu Asp Val Ala Gly Gly Thr Gly Asp Ile Ala Phe Arg Phe	
110 115 120	
ctt aat tat gtt cag tcc cag cat cag aga aaa cag aag agg cag tta	434
Leu Asn Tyr Val Gln Ser Gln His Gln Arg Lys Gln Lys Arg Gln Leu	
125 130 135 140	
agg gcc caa caa aat tta tcc tgg gaa gaa att gcc aaa gag tac cag	482
Arg Ala Gln Gln Asn Leu Ser Trp Glu Glu Ile Ala Lys Glu Tyr Gln	
145 150 155	
aat gaa gaa gat tcc ttg ggc ggg tct cgt gtc gtg gtg tgt gac atc	530
Asn Glu Glu Asp Ser Leu Gly Gly Ser Arg Val Val Val Cys Asp Ile	
160 165 170	
aac aag gag atg cta aag gtt gga aag cag aaa gcc ttg gct caa gga	578
Asn Lys Glu Met Leu Lys Val Gly Lys Gln Lys Ala Leu Ala Gln Gly	
175 180 185	
tac aga gct gga ctt gca tgg gta tta gga gat gct gaa gaa ctg ccc	626
Tyr Arg Ala Gly Leu Ala Trp Val Leu Gly Asp Ala Glu Glu Leu Pro	
190 195 200	

ttt gat gat gac aag ttt gat att tac acc att gcc ttt ggg atc cgg	674
Phe Asp Asp Asp Lys Phe Asp Ile Tyr Thr Ile Ala Phe Gly Ile Arg	
205 210 215 220	
aat gtc aca cac att gat cag gca ctc cag gaa gct cat cgg gtg ctg	722
Asn Val Thr His Ile Asp Gln Ala Leu Gln Glu Ala His Arg Val Leu	
225 230 235	
aaa cca gga gga cgg ttt ctc tgt ctg gaa ttt agc caa gtg aac aat	770
Lys Pro Gly Gly Arg Phe Leu Cys Leu Glu Phe Ser Gln Val Asn Asn	
240 245 250	
ccc ctc ata tcc agg ctt tat gat cta tat agc ttc cag gtc atc cct	818
Pro Leu Ile Ser Arg Leu Tyr Asp Leu Tyr Ser Phe Gln Val Ile Pro	
255 260 265	
gtc ctg gga gag gtc atc gct gga gac tgg aag tcc tat cag tac ctt	866
Val Leu Gly Glu Val Ile Ala Gly Asp Trp Lys Ser Tyr Gln Tyr Leu	
270 275 280	
gta gag agt atc cga agg ttt ccg tct cag gaa gag ttc aag gac atg	914
Val Glu Ser Ile Arg Arg Phe Pro Ser Gln Glu Glu Phe Lys Asp Met	
285 290 295 300	
ata gaa gat gca ggc ttt cac aag gtg act tac gaa agt cta aca tca	962
Ile Glu Asp Ala Gly Phe His Lys Val Thr Tyr Glu Ser Leu Thr Ser	
305 310 315	
ggc att gtg gcc att cat tct ggc ttc aaa ctt taa ttcctttcct	1008
Gly Ile Val Ala Ile His Ser Gly Phe Lys Leu	
320 325	
atcatggagc atgaaccagt catatcctgt tgaaagcctg gaactgaagg ataatctggc	1068
aaatgagaca gcagcagagc atctcctctt aaggatacgt gccttggaact catgtttgaa	1128
tcgaacagtc tcaaagtgga agaacaaatt cttgtcactt ttttacagct ttctttggag	1188
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aatgacaatt tttaaccaga aaatttaatt gtacctgaat caacctttca gcctaggacg	1428
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gagtttacct ttg	1502

<210> 40  
 <211> 327  
 <212> PRT  
 <213> Homo sapiens

<400> 40

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			20					25					30		
Trp	Pro	Gly	Asp	Leu	Leu	Ser	Ala	Arg	Leu	Leu	Ser	Gln	Glu	Lys	Arg
			35				40					45			
Ala	Ala	Glu	Thr	His	Phe	Gly	Phe	Glu	Thr	Val	Ser	Glu	Glu	Glu	Lys
			50			55					60				
Gly	Gly	Lys	Val	Tyr	Gln	Val	Phe	Glu	Ser	Val	Ala	Lys	Lys	Tyr	Asp
65					70					75					80
Val	Met	Asn	Asp	Met	Met	Ser	Leu	Gly	Ile	His	Arg	Val	Trp	Lys	Asp
				85					90					95	
Leu	Leu	Leu	Trp	Lys	Met	His	Pro	Leu	Pro	Gly	Thr	Gln	Leu	Leu	Asp
			100					105					110		
Val	Ala	Gly	Gly	Thr	Gly	Asp	Ile	Ala	Phe	Arg	Phe	Leu	Asn	Tyr	Val
			115				120					125			
Gln	Ser	Gln	His	Gln	Arg	Lys	Gln	Lys	Arg	Gln	Leu	Arg	Ala	Gln	Gln
			130			135					140				
Asn	Leu	Ser	Trp	Glu	Glu	Ile	Ala	Lys	Glu	Tyr	Gln	Asn	Glu	Glu	Asp
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Ser	Leu	Gly	Gly	Ser	Arg	Val	Val	Val	Cys	Asp	Ile	Asn	Lys	Glu	Met
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Leu	Lys	Val	Gly	Lys	Gln	Lys	Ala	Leu	Ala	Gln	Gly	Tyr	Arg	Ala	Gly
			180					185					190		
Leu	Ala	Trp	Val	Leu	Gly	Asp	Ala	Glu	Glu	Leu	Pro	Phe	Asp	Asp	Asp
			195				200					205			
Lys	Phe	Asp	Ile	Tyr	Thr	Ile	Ala	Phe	Gly	Ile	Arg	Asn	Val	Thr	His
			210			215					220				
Ile	Asp	Gln	Ala	Leu	Gln	Glu	Ala	His	Arg	Val	Leu	Lys	Pro	Gly	Gly
225					230					235					240
Arg	Phe	Leu	Cys	Leu	Glu	Phe	Ser	Gln	Val	Asn	Asn	Pro	Leu	Ile	Ser
			245						250					255	
Arg	Leu	Tyr	Asp	Leu	Tyr	Ser	Phe	Gln	Val	Ile	Pro	Val	Leu	Gly	Glu
			260					265					270		
Val	Ile	Ala	Gly	Asp	Trp	Lys	Ser	Tyr	Gln	Tyr	Leu	Val	Glu	Ser	Ile
			275				280					285			
Arg	Arg	Phe	Pro	Ser	Gln	Glu	Glu	Phe	Lys	Asp	Met	Ile	Glu	Asp	Ala
			290			295					300				
Gly	Phe	His	Lys	Val	Thr	Tyr	Glu	Ser	Leu	Thr	Ser	Gly	Ile	Val	Ala
305					310					315					320
Ile	His	Ser	Gly	Phe	Lys	Leu									
				325											

<210> 41  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (127)..(387)

<400> 41  
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 aaaacgctag agcggcgagt tgttacctgc gtcctctgac ctgagagcga aggggaaagc 120



Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
Male	55.2 (10.5)
Female	56.8 (11.2)
Marital status	
Married	78.5%
Single	21.5%
Education level	
High school or above	65.2%
Below high school	34.8%
Occupation	
White collar	45.1%
Blue collar	54.9%
Income (USD/month)	
< 1000	12.3%
1000-2000	35.7%
2000-3000	28.9%
> 3000	23.1%
Health insurance	
Yes	89.4%
No	10.6%
Comorbidities	
Hypertension	42.1%
Diabetes	18.5%
Cholesterol	31.2%
Smoking status	
Current smoker	15.3%
Former smoker	22.7%
Non-smoker	62.0%

51

ata aat gcc atg ttg gca atg agg aac taa gctgatattt aaatttcctg 641  
 Ile Asn Ala Met Leu Ala Met Arg Asn  
 170 175

ctttacacat gttataccat tgttttttcc ctcaagtatt ttttcctgt gaagaagatt 701  
 atttatctgc ttttatttta gtcactaaaa cttaaagtttt tattttttaca ttgtgatttt 761  
 tacattaataa tattaacttt ttttaagtct attttatgaa agattattgt aataaacttt 821  
 gatgggggtt gtatttttgt taatcttcat gaattgaata attgtttttt taaagcaaaa 881  
 taaagttttt taaataaatg tt 903

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 <211> 178  
 <212> PRT  
 <213> Homo sapiens

<400> 44  
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 Ala Gly Pro Gln Ala Gln Gln Ala Ala Arg Glu Val Asn Thr Ala Ser  
 20 25 30  
 Leu Cys Arg Ile Gly Gln Glu Thr Val Gln Asp Ile Val Tyr Arg Thr  
 35 40 45  
 Met Glu Ile Phe Gln Leu Leu Arg Asn Met Gln Leu Pro Asn Gly Val  
 50 55 60  
 Thr Tyr His Thr Gly Thr Tyr Gln Asp Arg Leu Thr Lys Leu Gln Asp  
 65 70 75 80  
 Asn Leu Arg Gln Leu Ser Val Leu Phe Arg Lys Leu Arg Leu Val Tyr  
 85 90 95  
 Asp Lys Cys Asn Glu Asn Cys Gly Gly Met Asp Pro Ile Pro Val Glu  
 100 105 110  
 Gln Leu Ile Pro Tyr Val Glu Glu Asp Gly Ser Lys Asn Asp Asp Arg  
 115 120 125  
 Ala Gly Pro Pro Arg Phe Ala Ser Glu Glu Arg Arg Glu Ile Ala Glu  
 130 135 140  
 Val Asn Lys Lys Leu Lys Gln Lys Asn Gln Gln Leu Lys Gln Ile Met  
 145 150 155 160  
 Asp Gln Leu Arg Asn Leu Ile Trp Asp Ile Asn Ala Met Leu Ala Met  
 165 170 175  
 Arg Asn

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<220>  
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gagaggaaaa tcccctgaat ccctgcagga ttaatttatt caaaaaggaa ataaaaaata 180

ctcaat atg caa aag tct tgt gaa gaa aat gag gga aaa cca cag aac 228  
Met Gln Lys Ser Cys Glu Glu Asn Glu Gly Lys Pro Gln Asn  
1 5 10

atg cca aag gcc gag gaa gat cgc cct ttg gag gat gta cca cag gag 276  
Met Pro Lys Ala Glu Glu Asp Arg Pro Leu Glu Asp Val Pro Gln Glu  
15 20 25 30

gca gaa gga aat cct caa cct tcc gaa gaa ggc gta agc cag gaa gca 324  
Ala Glu Gly Asn Pro Gln Pro Ser Glu Glu Gly Val Ser Gln Glu Ala  
35 40 45

gaa gga aac ccc aga gga ggg ccg aat cag cct ggc cag gga ttt aaa 372  
Glu Gly Asn Pro Arg Gly Gly Pro Asn Gln Pro Gly Gln Gly Phe Lys  
50 55 60

gag gac aca ccc gtt agg cat ttg gac cct gaa gaa atg ata aga gga 420  
Glu Asp Thr Pro Val Arg His Leu Asp Pro Glu Glu Met Ile Arg Gly  
65 70 75

gta gat gag ctt gaa agg ctt agg gaa gag ata aga aga gta aga aac 468  
Val Asp Glu Leu Glu Arg Leu Arg Glu Glu Ile Arg Arg Val Arg Asn  
80 85 90

aag ttt gtg atg atg cat tgg aag caa aga cat tca cgc agc cgt cct 516  
Lys Phe Val Met Met His Trp Lys Gln Arg His Ser Arg Ser Arg Pro  
95 100 105 110

tat cct gtg tgc ttt agg cct tga attcattttt gcctaataatt aaaatctggc 570  
Tyr Pro Val Cys Phe Arg Pro  
115

cccagctttc tttctgttag cattttctga tgtatctttg acctccattt tacttttaat 630

catctgatga aattttgttt taggtaattt ccttggtacc agcatctcat tggatttttg 690

attttgaccc attttccagg tctatttttc aattggaaac tttcacacat ttgcatggga 750

atatgttcat tccatgttgt aaagtaaaac ataacagggt atggcaaagc agcatattta 810

atatcagctc acatatgtag gataaaattc caaactttgt gtgtgtgct gtgtgtatac 870

atacatccat ataacatata tcacaaactt aaccaagctt atttctgtgt ggtgtgaaat 930

tttatttggt ttcttctttt tgttcttttt gcttatatgt actttttaat gaacacgtgt 990

ctcacacaca aaaagaatta aggatttttt ttacaagtaa gagtcaaata atttgcaacc 1050

agcttatgag ggcaatgggg gcacctaaac tcttgatgaa agaactttaa aaagaaatgt 1110

aaacctcaaa ttacctctgg atctcttagc cagaggaata aactggcaat tattacagat 1170

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 <211> 117  
 <212> PRT  
 <213> Homo sapiens

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 Lys Ala Glu Glu Asp Arg Pro Leu Glu Asp Val Pro Gln Glu Ala Glu  
 20 25 30  
 Gly Asn Pro Gln Pro Ser Glu Glu Gly Val Ser Gln Glu Ala Glu Gly  
 35 40 45  
 Asn Pro Arg Gly Gly Pro Asn Gln Pro Gly Gln Gly Phe Lys Glu Asp  
 50 55 60  
 Thr Pro Val Arg His Leu Asp Pro Glu Glu Met Ile Arg Gly Val Asp  
 65 70 75 80  
 Glu Leu Glu Arg Leu Arg Glu Glu Ile Arg Arg Val Arg Asn Lys Phe  
 85 90 95  
 Val Met Met His Trp Lys Gln Arg His Ser Arg Ser Arg Pro Tyr Pro  
 100 105 110  
 Val Cys Phe Arg Pro  
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<210> 47  
 <211> 404  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (105)..(365)

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 Met Glu Leu Ser  
 1  
 gcc gaa tac ctc cgc gag aag ctg cag cgg gac ctg gag gcg gag cat 164  
 Ala Glu Tyr Leu Arg Glu Lys Leu Gln Arg Asp Leu Glu Ala Glu His  
 5 10 15 20  
 gtg gag gtg gag gac acg acc ctc aac cgt tgc tcc tgt agc ttc cga 212  
 Val Glu Val Glu Asp Thr Thr Leu Asn Arg Cys Ser Cys Ser Phe Arg  
 25 30 35  
 gtc ctg gtg gtg tcg gcc aag ttc gag ggg aaa ccg ctg ctt cag aga 260  
 Val Leu Val Val Ser Ala Lys Phe Glu Gly Lys Pro Leu Leu Gln Arg  
 40 45 50  
 cac agg ctg gtg aac gcg tgc cta gca gaa gag ctc ccg cac atc cat 308  
 His Arg Leu Val Asn Ala Cys Leu Ala Glu Glu Leu Pro His Ile His  
 55 60 65

gcc ttt gaa cag aaa acc ctg acc cca gac cag tgg gca cgt gag cga 356  
Ala Phe Glu Gln Lys Thr Leu Thr Pro Asp Gln Trp Ala Arg Glu Arg  
70 75 80

cag aaa tga gggactggga tctgcacagc cattaaatta taaatctgg 404  
Gln Lys  
85

<210> 48  
<211> 86  
<212> PRT  
<213> Homo sapiens

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20 25 30  
Cys Ser Phe Arg Val Leu Val Val Ser Ala Lys Phe Glu Gly Lys Pro  
35 40 45  
Leu Leu Gln Arg His Arg Leu Val Asn Ala Cys Leu Ala Glu Glu Leu  
50 55 60  
Pro His Ile His Ala Phe Glu Gln Lys Thr Leu Thr Pro Asp Gln Trp  
65 70 75 80  
Ala Arg Glu Arg Gln Lys  
85

<210> 49  
<211> 752  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (95)..(634)

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Met Ala Ala Thr Glu Pro Ile  
1 5

ttg gcg gcc act ggg agt ccc gcg gcg gtg cca ccg gag aaa ctg gaa 163  
Leu Ala Ala Thr Gly Ser Pro Ala Ala Val Pro Pro Glu Lys Leu Glu  
10 15 20

gga gcc ggt tcg agc tca gcc cct gag cgt aac tgt gtg ggc tcc tcg 211  
Gly Ala Gly Ser Ser Ser Ala Pro Glu Arg Asn Cys Val Gly Ser Ser  
25 30 35

ctg cca gag gcc tca ccg cct gcc cct gag cct tcc agt ccc aac gcc 259  
Leu Pro Glu Ala Ser Pro Pro Ala Pro Glu Pro Ser Ser Pro Asn Ala  
40 45 50 55



Gln Phe Arg Tyr Gln Asp Ala Ala Gly Pro Arg Glu Ala Phe Arg Gln  
 115 120 125  
 Leu Arg Glu Leu Ser Arg Gln Trp Leu Arg Pro Asp Ile Arg Thr Lys  
 130 135 140  
 Glu Gln Ile Val Glu Met Leu Val Gln Glu Gln Leu Leu Ala Ile Leu  
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 Ile Thr Gly

<210> 51  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (219)..(788)

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 ctgaccgcgt gatccgcccg cctcggcctc cgaaactgct gaaattacag gcgtgagcca 180  
 ccgcgcccgg ccctccctct tccgctgccg ccgtggga atg gaa aca tct gcc cca 236  
 Met Glu Thr Ser Ala Pro  
 1 5  
 cgt gcc gga agc caa gtg gtg gcg aca act gcg cgc cac tcc gcg gcc 284  
 Arg Ala Gly Ser Gln Val Val Ala Thr Thr Ala Arg His Ser Ala Ala  
 10 15 20  
 tac cgc gca gat cct cta cgt gtg tcc tcg cga gac aag ctc acc gaa 332  
 Tyr Arg Ala Asp Pro Leu Arg Val Ser Ser Arg Asp Lys Leu Thr Glu  
 25 30 35  
 atg gcc gcg tcc agt caa gga aac ttt gag gga aat ttt gag tca ctg 380  
 Met Ala Ala Ser Ser Gln Gly Asn Phe Glu Gly Asn Phe Glu Ser Leu  
 40 45 50  
 gac ctt gcg gaa ttt gct aag aag cag cca tgg tgg cgt aag ctg ttc 428  
 Asp Leu Ala Glu Phe Ala Lys Lys Gln Pro Trp Trp Arg Lys Leu Phe  
 55 60 65 70  
 ggg cag gaa tct gga cct tca gca gaa aag tat agc gtg gca acc cag 476  
 Gly Gln Glu Ser Gly Pro Ser Ala Glu Lys Tyr Ser Val Ala Thr Gln  
 75 80 85  
 ctg ttc att gga ggt gtc act gga tgg tgc aca ggt ttc ata ttc cag 524  
 Leu Phe Ile Gly Gly Val Thr Gly Trp Cys Thr Gly Phe Ile Phe Gln  
 90 95 100  
 aag gtt gga aag ttg gct gca aca gct gtg gga ggt gga ttt ttt ctc 572  
 Lys Val Gly Lys Leu Ala Ala Thr Ala Val Gly Gly Gly Phe Phe Leu

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105              110              115
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Leu Gln Leu Ala Asn His Thr Gly Tyr Ile Lys Val Asp Trp Gln Arg
120              125              130

gtg gag aag gac atg aag aaa gcc aaa gag cag ctg aag atc cgt aag 668
Val Glu Lys Asp Met Lys Lys Ala Lys Glu Gln Leu Lys Ile Arg Lys
135              140              145

agc aat cag ata cct act gag gtc agg agc aaa gct gag gag gtg gtg 716
Ser Asn Gln Ile Pro Thr Glu Val Arg Ser Lys Ala Glu Glu Val Val
155              160              165

tca ttt gtg aag aag aat gtt cta gta act ggg gga ttt ttc gga ggc 764
Ser Phe Val Lys Lys Asn Val Leu Val Thr Gly Gly Phe Phe Gly Gly
170              175              180

ttt ctg ctt ggc atg gca tcc taa ggaagatgac ctcattgttca ttgttcctgg 818
Phe Leu Leu Gly Met Ala Ser
185

ttttttccag ccagcagcct ctacactcca tcataggaca tcgagtcctt cctcctcttc 878

tcccatgcct tcttcctgc catggcaaatt ctgagtggtt tctctaagca tctgctggta 938

caagtcaatg tggcaccatg agcttcatgg tggcagaaga gacaatagtc cttagctctc 998

ctcccagtac accccctact tggccagtct gtaggccaac aagaaggttc ctttaccctc 1058

atgcaagaca cttatgagaa cacattacaa gatggctgac cgtggaggat gaggggatcc 1118

tgaaagggttg tcccaaactg ttgatttgga aaagaaataa gcacatagat aaccttattg 1178

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 <211> 189  
 <212> PRT  
 <213> Homo sapiens

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Ala Arg His Ser Ala Ala Tyr Arg Ala Asp Pro Leu Arg Val Ser Ser
20     25     30
Arg Asp Lys Leu Thr Glu Met Ala Ala Ser Ser Gln Gly Asn Phe Glu
35     40     45
Gly Asn Phe Glu Ser Leu Asp Leu Ala Glu Phe Ala Lys Lys Gln Pro
50     55     60
Trp Trp Arg Lys Leu Phe Gly Gln Glu Ser Gly Pro Ser Ala Glu Lys
65     70     75     80
Tyr Ser Val Ala Thr Gln Leu Phe Ile Gly Gly Val Thr Gly Trp Cys
85     90     95
Thr Gly Phe Ile Phe Gln Lys Val Gly Lys Leu Ala Ala Thr Ala Val
100    105    110

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Gly Gly Gly Phe Phe Leu Leu Gln Leu Ala Asn His Thr Gly Tyr Ile  
 115 120 125  
 Lys Val Asp Trp Gln Arg Val Glu Lys Asp Met Lys Lys Ala Lys Glu  
 130 135 140  
 Gln Leu Lys Ile Arg Lys Ser Asn Gln Ile Pro Thr Glu Val Arg Ser  
 145 150 155 160  
 Lys Ala Glu Glu Val Val Ser Phe Val Lys Lys Asn Val Leu Val Thr  
 165 170 175  
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 180 185

<210> 53  
 <211> 1209  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (95)..(448)

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 Met Ile Ser Gly Leu Phe Met  
 1 5  
 tcg ttg tgc tgc gcc ggg agc cac cgc cct ccg gag aca ggg cag ctc 163  
 Ser Leu Cys Cys Ala Gly Ser His Arg Pro Pro Glu Thr Gly Gln Leu  
 10 15 20  
 ccc tac gac cct agc gcc tcc gcc ctc cgc ggc ccc tct cct ctc ttc 211  
 Pro Tyr Asp Pro Ser Ala Ser Ala Leu Arg Gly Pro Ser Pro Leu Phe  
 25 30 35  
 ctg ctc tgt ccc tcc ttc tcc atc agg gag cag cgt gac ttc agc gag 259  
 Leu Leu Cys Pro Ser Phe Ser Ile Arg Glu Gln Arg Asp Phe Ser Glu  
 40 45 50 55  
 tcc cgc gag cac ctg gct aga cag tta aca agc acg tcc ttc cag cct 307  
 Ser Arg Glu His Leu Ala Arg Gln Leu Thr Ser Thr Ser Phe Gln Pro  
 60 65 70  
 gag cca gcg cag gtt tgg gag ggg gct tcc tgg ccc ccc cca cgg tgt 355  
 Glu Pro Ala Gln Val Trp Glu Gly Ala Ser Trp Pro Pro Pro Arg Cys  
 75 80 85  
 tcc agc ccc tcc tct ctt ccg ccc cct agt ctc cca ccc ttc cct ccc 403  
 Ser Ser Pro Ser Ser Leu Pro Pro Pro Ser Leu Pro Pro Phe Pro Pro  
 90 95 100  
 cgt agt gac caa ttc cta tct ctt ccc tct ccg cag gct caa tga 448  
 Arg Ser Asp Gln Phe Leu Ser Leu Pro Ser Pro Gln Ala Gln  
 105 110 115  
 atcgaatgaa tgtgaacttc ttcattctgtg aaaaatcttt tttttttcca ttttgttctg 508

09890688-093761

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 <211> 117  
 <212> PRT  
 <213> Homo sapiens

<400> 54  
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 Pro Pro Glu Thr Gly Gln Leu Pro Tyr Asp Pro Ser Ala Ser Ala Leu  
 20 25 30  
 Arg Gly Pro Ser Pro Leu Phe Leu Leu Cys Pro Ser Phe Ser Ile Arg  
 35 40 45  
 Glu Gln Arg Asp Phe Ser Glu Ser Arg Glu His Leu Ala Arg Gln Leu  
 50 55 60  
 Thr Ser Thr Ser Phe Gln Pro Glu Pro Ala Gln Val Trp Glu Gly Ala  
 65 70 75 80  
 Ser Trp Pro Pro Pro Arg Cys Ser Ser Pro Ser Ser Leu Pro Pro Pro  
 85 90 95  
 Ser Leu Pro Pro Phe Pro Pro Arg Ser Asp Gln Phe Leu Ser Leu Pro  
 100 105 110  
 Ser Pro Gln Ala Gln  
 115

<210> 55  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS

<222> (26)..(922)

<400> 55

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			1					5								
gta	ttc	aaa	gtg	gga	aac	cgc	ttc	cag	acg	gcg	cgt	ttc	tat	cgg	gac	100
Val	Phe	Lys	Val	Gly	Asn	Arg	Phe	Gln	Thr	Ala	Arg	Phe	Tyr	Arg	Asp	
10				15						20					25	
gtc	ctg	ggg	atg	aag	gtt	ctg	cgg	cat	gag	gaa	ttt	gaa	gaa	ggc	tgc	148
Val	Leu	Gly	Met	Lys	Val	Leu	Arg	His	Glu	Glu	Phe	Glu	Glu	Gly	Cys	
				30					35					40		
aaa	gct	gcc	tgt	aat	ggg	cct	tat	gat	ggg	aaa	tgg	agt	aaa	aca	atg	196
Lys	Ala	Ala	Cys	Asn	Gly	Pro	Tyr	Asp	Gly	Lys	Trp	Ser	Lys	Thr	Met	
			45					50					55			
gtg	gga	ttt	ggg	cct	gag	gat	gat	cat	ttt	gtc	gca	gaa	ctg	act	tac	244
Val	Gly	Phe	Gly	Pro	Glu	Asp	Asp	His	Phe	Val	Ala	Glu	Leu	Thr	Tyr	
		60					65					70				
aat	tat	ggc	gtc	gga	gac	tac	aag	ctt	ggc	aat	gac	ttt	atg	gga	atc	292
Asn	Tyr	Gly	Val	Gly	Asp	Tyr	Lys	Leu	Gly	Asn	Asp	Phe	Met	Gly	Ile	
	75					80					85					
acg	ctc	gct	tct	agc	cag	gct	gtc	agc	aac	gcc	agg	aag	ctg	gag	tgg	340
Thr	Leu	Ala	Ser	Ser	Gln	Ala	Val	Ser	Asn	Ala	Arg	Lys	Leu	Glu	Trp	
90					95					100					105	
cca	ctg	acg	gaa	gtt	gca	gaa	ggt	gtt	ttt	gaa	acc	gag	gcc	ccg	gga	388
Pro	Leu	Thr	Glu	Val	Ala	Glu	Gly	Val	Phe	Glu	Thr	Glu	Ala	Pro	Gly	
				110					115					120		
gga	tat	aag	ttc	tat	ttg	cag	aat	cgc	agt	ctg	cct	cag	tca	gat	cct	436
Gly	Tyr	Lys	Phe	Tyr	Leu	Gln	Asn	Arg	Ser	Leu	Pro	Gln	Ser	Asp	Pro	
			125					130				135				
gta	tta	aaa	gta	act	cta	gca	gtg	tct	gat	ctt	caa	aag	tcc	ttg	aac	484
Val	Leu	Lys	Val	Thr	Leu	Ala	Val	Ser	Asp	Leu	Gln	Lys	Ser	Leu	Asn	
		140					145					150				
tac	tgg	tgt	aat	cta	ctg	gga	atg	aaa	att	tat	gaa	aaa	gat	gaa	gaa	532
Tyr	Trp	Cys	Asn	Leu	Leu	Gly	Met	Lys	Ile	Tyr	Glu	Lys	Asp	Glu	Glu	
	155					160					165					
aag	caa	agg	gct	ttg	ctg	ggc	tat	gct	gat	aac	cag	tgt	aag	ctg	gag	580
Lys	Gln	Arg	Ala	Leu	Leu	Gly	Tyr	Ala	Asp	Asn	Gln	Cys	Lys	Leu	Glu	
170					175					180					185	
cta	cag	ggc	gtc	aag	ggg	ggg	gtg	gac	cat	gca	gca	gct	ttt	gga	aga	628
Leu	Gln	Gly	Val	Lys	Gly	Gly	Val	Asp	His	Ala	Ala	Ala	Phe	Gly	Arg	
				190					195					200		
att	gcc	ttc	tct	tgc	ccc	cag	aaa	gag	ttg	cca	gac	tta	gaa	gac	ttg	676
Ile	Ala	Phe	Ser	Cys	Pro	Gln	Lys	Glu	Leu	Pro	Asp	Leu	Glu	Asp	Leu	

205	210	215	
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Met Lys Arg Glu Asn Gln Lys Ile Leu Thr Pro Leu Val Ser Leu Asp			
220	225	230	
acc cca ggg aaa gca aca gta cag gtg gtc att ctg gcc gac cct gac			772
Thr Pro Gly Lys Ala Thr Val Gln Val Val Ile Leu Ala Asp Pro Asp			
235	240	245	
gga cat gaa att tgc ttt gtc ggg gat gaa gca ttt cga gaa ctt tct			820
Gly His Glu Ile Cys Phe Val Gly Asp Glu Ala Phe Arg Glu Leu Ser			
250	255	260	265
aag atg gat cca gag gga agc aaa ttg ttg gat gat gca atg gca gca			868
Lys Met Asp Pro Glu Gly Ser Lys Leu Leu Asp Asp Ala Met Ala Ala			
270	275	280	
gat aaa agt gac gag tgg ttt gcc aaa cac aat aaa ccc aaa gct tca			916
Asp Lys Ser Asp Glu Trp Phe Ala Lys His Asn Lys Pro Lys Ala Ser			
285	290	295	
ggt taa cggaagacat gatgcagagc aagcctctgt gattcctgcc cagcacctgt			972
Gly			
gaggcctgac gtgtcagttc ccaataaatg ctcttctgat ttgtttcccg tacaggcaag			1032
gaggcttggg tagtgcagat ttgtgtatatt caatctttga aagctctgat gtaatttaga			1092
aatgaaatcc aatcatgagt ccaggtagag aacgcctgct gtaatctaca ctgttgctgg			1152
gactgcgcat tctgtatata actgtgttgg atgagtgaca gatgattgtc cagactagga			1212
cagcggcatg aacatgactt tggttgggat tgcggatagt tagggttacc tctgaatcgt			1272
gtagctttta tgagagcagc tgtgcaagtg aatccacatt aatgccttgt cgtgggtgcc			1332
ttcccagcgc ctgacgatac gctcttctat tgtcttattc tggcaggttt tgacgtttta			1392
aattttttta agaaatttta ttccttgagc caaaagggtt ggtaaccac cccctctta			1452
cttgctttca cattttgagt gtccagagga aacagaaaagg aatgagtgtg tgacgttgct			1512
gcacgcctga ctctgtgcga gcttctttct gtgtatatat tttgttttat tttttccgt			1572
gtatatatttt aatcccgaca gaacatcatg tgagatttct ttaaaatgga ttaaacgatt			1632
tcttcagcct gaaaaaaaag gttttgaaaa tgttttcttg tagttttgtt tggttctaaa			1692
caacaaatag gttttaatca ctcgaaatgg aatttatattg tgtattcatt gaataaattt			1752
tttttgaaag t			1763
<210> 56			
<211> 298			
<212> PRT			

<213> Homo sapiens

<400> 56

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Phe Gln Thr Ala Arg Phe Tyr Arg Asp Val Leu Gly Met Lys Val Leu  
20 25 30  
Arg His Glu Glu Phe Glu Glu Gly Cys Lys Ala Ala Cys Asn Gly Pro  
35 40 45  
Tyr Asp Gly Lys Trp Ser Lys Thr Met Val Gly Phe Gly Pro Glu Asp  
50 55 60  
Asp His Phe Val Ala Glu Leu Thr Tyr Asn Tyr Gly Val Gly Asp Tyr  
65 70 75 80  
Lys Leu Gly Asn Asp Phe Met Gly Ile Thr Leu Ala Ser Ser Gln Ala  
85 90 95  
Val Ser Asn Ala Arg Lys Leu Glu Trp Pro Leu Thr Glu Val Ala Glu  
100 105 110  
Gly Val Phe Glu Thr Glu Ala Pro Gly Gly Tyr Lys Phe Tyr Leu Gln  
115 120 125  
Asn Arg Ser Leu Pro Gln Ser Asp Pro Val Leu Lys Val Thr Leu Ala  
130 135 140  
Val Ser Asp Leu Gln Lys Ser Leu Asn Tyr Trp Cys Asn Leu Leu Gly  
145 150 155 160  
Met Lys Ile Tyr Glu Lys Asp Glu Glu Lys Gln Arg Ala Leu Leu Gly  
165 170 175  
Tyr Ala Asp Asn Gln Cys Lys Leu Glu Leu Gln Gly Val Lys Gly Gly  
180 185 190  
Val Asp His Ala Ala Ala Phe Gly Arg Ile Ala Phe Ser Cys Pro Gln  
195 200 205  
Lys Glu Leu Pro Asp Leu Glu Asp Leu Met Lys Arg Glu Asn Gln Lys  
210 215 220  
Ile Leu Thr Pro Leu Val Ser Leu Asp Thr Pro Gly Lys Ala Thr Val  
225 230 235 240  
Gln Val Val Ile Leu Ala Asp Pro Asp Gly His Glu Ile Cys Phe Val  
245 250 255  
Gly Asp Glu Ala Phe Arg Glu Leu Ser Lys Met Asp Pro Glu Gly Ser  
260 265 270  
Lys Leu Leu Asp Asp Ala Met Ala Ala Asp Lys Ser Asp Glu Trp Phe  
275 280 285  
Ala Lys His Asn Lys Pro Lys Ala Ser Gly  
290 295

<210> 57

<211> 1913

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (303)..(1379)

<400> 57

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acagagagag agggatagct aaaactacgt gagcctggcg aggggtgcaga gcagaaagta 120

gagactgtcc gaagactgct atctgggacg agacaagttg ttaaagggac aggagagaaa 180  
gcagagctat ttcaagagtg agccacagaa gggaatccag aggccatcta agcgaggaag 240  
ggctctacagg cagtgagtga aggccaggag cagggcccag gccaggcacg accaccgagg 300  
gg atg aac ttc aca gtg ggt ttc aag ccg ctg cta ggg gat gca cac 347  
Met Asn Phe Thr Val Gly Phe Lys Pro Leu Leu Gly Asp Ala His  
1 5 10 15  
agc atg gac aac ctg gag aag cag ctc atc tgc ccc atc tgc ctg gag 395  
Ser Met Asp Asn Leu Glu Lys Gln Leu Ile Cys Pro Ile Cys Leu Glu  
20 25 30  
atg ttc tcc aaa cca gtg gtg atc ctg ccc tgc caa cac aac ctg tgc 443  
Met Phe Ser Lys Pro Val Val Ile Leu Pro Cys Gln His Asn Leu Cys  
35 40 45  
cgc aaa tgt gcc aac gac gtc ttc cag gcc tcg aat cct cta tgg cag 491  
Arg Lys Cys Ala Asn Asp Val Phe Gln Ala Ser Asn Pro Leu Trp Gln  
50 55 60  
tcc cgg ggc tcc acc act gtg tct tca gga ggc cgt ttc cgc tgc cca 539  
Ser Arg Gly Ser Thr Thr Val Ser Ser Gly Gly Arg Phe Arg Cys Pro  
65 70 75  
tcg tgc agg cat gag gtt gtc ctg gac aga cac ggt gtc tac ggc ctg 587  
Ser Cys Arg His Glu Val Val Leu Asp Arg His Gly Val Tyr Gly Leu  
80 85 90 95  
cag cga aac ctg cta gtg gag aac att atc gac att tac aag cag gag 635  
Gln Arg Asn Leu Val Glu Asn Ile Ile Asp Ile Tyr Lys Gln Glu  
100 105 110  
tca tcc agg ccg ctg cac tcc aag gct gag cag cac ctc atg tgc gag 683  
Ser Ser Arg Pro Leu His Ser Lys Ala Glu Gln His Leu Met Cys Glu  
115 120 125  
gag cat gaa gaa gag aag atc aat att tac tgc ctg agc tgt gag gtg 731  
Glu His Glu Glu Glu Lys Ile Asn Ile Tyr Cys Leu Ser Cys Glu Val  
130 135 140  
ccc acc tgc tct ctc tgc aag gtc ttc ggt gcc cac aag gac tgt gag 779  
Pro Thr Cys Ser Leu Cys Lys Val Phe Gly Ala His Lys Asp Cys Glu  
145 150 155  
gtg gcc cca ctg ccc acc att tac aaa cgc cag aag agt gag ctc agc 827  
Val Ala Pro Leu Pro Thr Ile Tyr Lys Arg Gln Lys Ser Glu Leu Ser  
160 165 170 175  
gat ggc atc gcg atg ctg gtg gca ggc aat gac cgc gtg caa gca gtg 875  
Asp Gly Ile Ala Met Leu Val Ala Gly Asn Asp Arg Val Gln Ala Val  
180 185 190  
atc aca cag atg gag gag gtg tgc cag act atc gag gac aat agc cgg 923  
Ile Thr Gln Met Glu Glu Val Cys Gln Thr Ile Glu Asp Asn Ser Arg

195	200	205	
agg cag aag cag ttg tta aac cag agg ttt gag agc ctg tgc gca gtg			971
Arg Gln Lys Gln Leu Leu Asn Gln Arg Phe Glu Ser Leu Cys Ala Val			
210	215	220	
ctg gag gag cgc aag ggt gag ctg ctg cag gcg ctg gcc cgg gag caa			1019
Leu Glu Glu Arg Lys Gly Glu Leu Leu Gln Ala Leu Ala Arg Glu Gln			
225	230	235	
gag gag aag ctg cag cgc gtc cgc ggc ctc atc cgt cag tat ggc gac			1067
Glu Glu Lys Leu Gln Arg Val Arg Gly Leu Ile Arg Gln Tyr Gly Asp			
240	245	250	255
cac ctg gag gcc tcc tct aag ctg gtg gag tct gcc atc cag tcc atg			1115
His Leu Glu Ala Ser Ser Lys Leu Val Glu Ser Ala Ile Gln Ser Met			
260	265	270	
gaa gag cca caa atg gcg ctg tat ctc cag cag gcc aag gag ctg atc			1163
Glu Glu Pro Gln Met Ala Leu Tyr Leu Gln Gln Ala Lys Glu Leu Ile			
275	280	285	
aat aag gtc ggg gcc atg tcg aag gtg gag ctg gca ggg cgg ccg gag			1211
Asn Lys Val Gly Ala Met Ser Lys Val Glu Leu Ala Gly Arg Pro Glu			
290	295	300	
cca ggc tat gag agc atg gag caa ttc acc gta agg gtg gag cac gtg			1259
Pro Gly Tyr Glu Ser Met Glu Gln Phe Thr Val Arg Val Glu His Val			
305	310	315	
gcc gaa atg ctg cgg acc atc gac ttc cag cca ggc gct tcc ggg gag			1307
Ala Glu Met Leu Arg Thr Ile Asp Phe Gln Pro Gly Ala Ser Gly Glu			
320	325	330	335
gaa gag gag gtg gcc cca gac gga gag gag ggc agc gcg ggg ccg gag			1355
Glu Glu Glu Val Ala Pro Asp Gly Glu Glu Gly Ser Ala Gly Pro Glu			
340	345	350	
gaa gag cgg ccg gat ggg cct taa ggccctgcgcc gacccgaccc tgctcgagag			1409
Glu Glu Arg Pro Asp Gly Pro			
355			
cccgcgctag agtcgggggag gatctgcgca gagaccgcag catcacccaa atcggcgccg			1469
gccccgggag gatctcaata aagaactcga gcgtcccaga cccgtatctc ctttcgctgc			1529
ccaaccccgcc agcctgggct tcgaaggcga cccgcccacc atcctgccct tcccagaacc			1589
tgagaccgtc tggggggcg aagccaaatg aaccctatt gggcacctct gtgatgccag			1649
gagcgaactg gtgagcccag cgccctggga agagggccga gggcggggag gtggtgccgg			1709
gacctctgag gtccctggga tttggggacc cttgggggtcc acatgcacct ggctgacctg			1769
gctgaaagcc gctgtctcgg agccccccac agcattttgt tcccctcccg ctggccccggg			1829
ggccccacct tcccacgggt tcccacgctg ctgtgactgc cctgcctcta cgacaaaagc			1889

caacgggtct tcagtacttt tatt

1913

<210> 58  
 <211> 358  
 <212> PRT  
 <213> Homo sapiens

<400> 58  
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 Met Asp Asn Leu Glu Lys Gln Leu Ile Cys Pro Ile Cys Leu Glu Met  
 20 25 30  
 Phe Ser Lys Pro Val Val Ile Leu Pro Cys Gln His Asn Leu Cys Arg  
 35 40 45  
 Lys Cys Ala Asn Asp Val Phe Gln Ala Ser Asn Pro Leu Trp Gln Ser  
 50 55 60  
 Arg Gly Ser Thr Thr Val Ser Ser Gly Gly Arg Phe Arg Cys Pro Ser  
 65 70 75 80  
 Cys Arg His Glu Val Val Leu Asp Arg His Gly Val Tyr Gly Leu Gln  
 85 90 95  
 Arg Asn Leu Leu Val Glu Asn Ile Ile Asp Ile Tyr Lys Gln Glu Ser  
 100 105 110  
 Ser Arg Pro Leu His Ser Lys Ala Glu Gln His Leu Met Cys Glu Glu  
 115 120 125  
 His Glu Glu Glu Lys Ile Asn Ile Tyr Cys Leu Ser Cys Glu Val Pro  
 130 135 140  
 Thr Cys Ser Leu Cys Lys Val Phe Gly Ala His Lys Asp Cys Glu Val  
 145 150 155 160  
 Ala Pro Leu Pro Thr Ile Tyr Lys Arg Gln Lys Ser Glu Leu Ser Asp  
 165 170 175  
 Gly Ile Ala Met Leu Val Ala Gly Asn Asp Arg Val Gln Ala Val Ile  
 180 185 190  
 Thr Gln Met Glu Glu Val Cys Gln Thr Ile Glu Asp Asn Ser Arg Arg  
 195 200 205  
 Gln Lys Gln Leu Leu Asn Gln Arg Phe Glu Ser Leu Cys Ala Val Leu  
 210 215 220  
 Glu Glu Arg Lys Gly Glu Leu Leu Gln Ala Leu Ala Arg Glu Gln Glu  
 225 230 235 240  
 Glu Lys Leu Gln Arg Val Arg Gly Leu Ile Arg Gln Tyr Gly Asp His  
 245 250 255  
 Leu Glu Ala Ser Ser Lys Leu Val Glu Ser Ala Ile Gln Ser Met Glu  
 260 265 270  
 Glu Pro Gln Met Ala Leu Tyr Leu Gln Gln Ala Lys Glu Leu Ile Asn  
 275 280 285  
 Lys Val Gly Ala Met Ser Lys Val Glu Leu Ala Gly Arg Pro Glu Pro  
 290 295 300  
 Gly Tyr Glu Ser Met Glu Gln Phe Thr Val Arg Val Glu His Val Ala  
 305 310 315 320  
 Glu Met Leu Arg Thr Ile Asp Phe Gln Pro Gly Ala Ser Gly Glu Glu  
 325 330 335  
 Glu Glu Val Ala Pro Asp Gly Glu Glu Gly Ser Ala Gly Pro Glu Glu  
 340 345 350  
 Glu Arg Pro Asp Gly Pro  
 355

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170	175	180	
ctg gga gca gga tcc tta ctt ctt gtc atc acc tac cca cta atg aaa			628
Leu Gly Ala Gly Ser Leu Leu Leu Val Ile Thr Tyr Pro Leu Met Lys			
185	190	195	
aga att tca tac tgg cct caa cta gcc ttg ggc ttg aca ttt aat tgg			676
Arg Ile Ser Tyr Trp Pro Gln Leu Ala Leu Gly Leu Thr Phe Asn Trp			
200	205	210	215
gga gcg tta ctt gga tgg tct gct atc aag ggt tcc tgt gat cca tct			724
Gly Ala Leu Leu Gly Trp Ser Ala Ile Lys Gly Ser Cys Asp Pro Ser			
	220	225	230
gtt tgc ctg cct ctt tat ttt tct gga gtt atg tgg aca cta ata tat			772
Val Cys Leu Pro Leu Tyr Phe Ser Gly Val Met Trp Thr Leu Ile Tyr			
	235	240	245
gac act att tat gcc cat cag gac aaa aga gat gat gtt ttg att ggt			820
Asp Thr Ile Tyr Ala His Gln Asp Lys Arg Asp Asp Val Leu Ile Gly			
	250	255	260
ctt aag tca acg gct ctg cgg ttc gga gaa aat acc aag ccg tgg ctc			868
Leu Lys Ser Thr Ala Leu Arg Phe Gly Glu Asn Thr Lys Pro Trp Leu			
	265	270	275
agc ggc ttc agt gtt gca atg ctg ggg gca ctg agc cta gtg ggt gtg			916
Ser Gly Phe Ser Val Ala Met Leu Gly Ala Leu Ser Leu Val Gly Val			
280	285	290	295
aac agt gga cag act gct ccc tac tac gct gcc ctg ggt gct gta gga			964
Asn Ser Gly Gln Thr Ala Pro Tyr Tyr Ala Ala Leu Gly Ala Val Gly			
	300	305	310
gcc cat ctg act cac cag att tac act cta gac atc cac aga cct gag			1012
Ala His Leu Thr His Gln Ile Tyr Thr Leu Asp Ile His Arg Pro Glu			
	315	320	325
gat tgt tgg aat aaa ttt atc tcc aac cga aca ctg gga cta ata gtt			1060
Asp Cys Trp Asn Lys Phe Ile Ser Asn Arg Thr Leu Gly Leu Ile Val			
	330	335	340
ttt tta ggg att gtc ctt ggg aat ttg tgg aaa gaa aag aag aca gac			1108
Phe Leu Gly Ile Val Leu Gly Asn Leu Trp Lys Glu Lys Lys Thr Asp			
	345	350	355
aaa aca aag aag ggt ata gag aat aaa ata gaa aat taa tgaatgaaat			1157
Lys Thr Lys Lys Gly Ile Glu Asn Lys Ile Glu Asn			
360	365	370	
ttatctagga atttttaaaa catttttttac aaaatataat tagatttgaa tacaaaatct			1217
gatacaatat gttaaagaat taagaacctg aagatgaaga tttagagcat atttacctgg			1277
attttactta tttgctagca aaattccccc ttgtcacaga aaccagggac tcttcaggat			1337
ttgagatggc cttgagtatt ttagttgata cattcttctg ccattataa ttctcacctg			1397

aagttatggg gattgcacag gttttggcac ttttagaaaa gcctgatgtg ggtcttacat 1457

aaatgaatgt ctgtataaga aaatggactc ttttttttag ggaaaaataa aagcaactat 1517

ggg 1520

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<211> 371  
<212> PRT  
<213> Homo sapiens

<400> 60  
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Ala Leu Ala Trp Leu Pro Gly Trp Arg Gly Arg Ser Phe Ala Leu Ala  
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Arg Ala Ala Gly Ala Pro His Gly Gly Asp Leu Gln Pro Pro Ala Cys  
35 40 45  
Pro Glu Pro Arg Gly Arg Gln Leu Ser Leu Ser Ala Ala Ala Val Val  
50 55 60  
Asp Ser Ala Pro Arg Pro Leu Gln Pro Tyr Leu Arg Leu Met Arg Leu  
65 70 75 80  
Asp Lys Pro Ile Gly Thr Trp Leu Leu Tyr Leu Pro Cys Thr Trp Ser  
85 90 95  
Ile Gly Leu Ala Ala Glu Pro Gly Cys Phe Pro Asp Trp Tyr Met Leu  
100 105 110  
Ser Leu Phe Gly Thr Gly Ala Ile Leu Met Arg Gly Ala Gly Cys Thr  
115 120 125  
Ile Asn Asp Met Trp Asp Gln Asp Tyr Asp Lys Lys Val Thr Arg Thr  
130 135 140  
Ala Asn Arg Pro Ile Ala Ala Gly Asp Ile Ser Thr Phe Gln Ser Phe  
145 150 155 160  
Val Phe Leu Gly Gly Gln Leu Thr Leu Ala Leu Gly Val Leu Leu Cys  
165 170 175  
Leu Asn Tyr Tyr Ser Ile Ala Leu Gly Ala Gly Ser Leu Leu Leu Val  
180 185 190  
Ile Thr Tyr Pro Leu Met Lys Arg Ile Ser Tyr Trp Pro Gln Leu Ala  
195 200 205  
Leu Gly Leu Thr Phe Asn Trp Gly Ala Leu Leu Gly Trp Ser Ala Ile  
210 215 220  
Lys Gly Ser Cys Asp Pro Ser Val Cys Leu Pro Leu Tyr Phe Ser Gly  
225 230 235 240  
Val Met Trp Thr Leu Ile Tyr Asp Thr Ile Tyr Ala His Gln Asp Lys  
245 250 255  
Arg Asp Asp Val Leu Ile Gly Leu Lys Ser Thr Ala Leu Arg Phe Gly  
260 265 270  
Glu Asn Thr Lys Pro Trp Leu Ser Gly Phe Ser Val Ala Met Leu Gly  
275 280 285  
Ala Leu Ser Leu Val Gly Val Asn Ser Gly Gln Thr Ala Pro Tyr Tyr  
290 295 300  
Ala Ala Leu Gly Ala Val Gly Ala His Leu Thr His Gln Ile Tyr Thr  
305 310 315 320  
Leu Asp Ile His Arg Pro Glu Asp Cys Trp Asn Lys Phe Ile Ser Asn  
325 330 335  
Arg Thr Leu Gly Leu Ile Val Phe Leu Gly Ile Val Leu Gly Asn Leu

340                      345                      350  
 Trp Lys Glu Lys Lys Thr Asp Lys Thr Lys Lys Gly Ile Glu Asn Lys  
           355                      360                      365  
 Ile Glu Asn  
           370

<210> 61  
 <211> 1731  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (183)..(1301)

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 cagcattgtg ttagtgccgg gaggccactg tgtcagcaag ctgagagggga aactgaagca 180  
 ag atg tcg ggc cgg agt ggg aag aag aaa atg tcc aag ctg tcc cgt 227  
   Met Ser Gly Arg Ser Gly Lys Lys Lys Met Ser Lys Leu Ser Arg  
       1                      5                      10                      15  
 tca gct agg gca ggt gtc atc ttt cca gtg ggg agg ctg atg cgt tat 275  
 Ser Ala Arg Ala Gly Val Ile Phe Pro Val Gly Arg Leu Met Arg Tyr  
                           20                      25                      30  
 ctg aag aaa ggg acg ttc aag tac cgg atc agc gtg ggc gcc cct gtc 323  
 Leu Lys Lys Gly Thr Phe Lys Tyr Arg Ile Ser Val Gly Ala Pro Val  
                           35                      40                      45  
 tac atg gcg gca gtc att gag tac ctg gca gcg gaa att cta gaa ttg 371  
 Tyr Met Ala Ala Val Ile Glu Tyr Leu Ala Ala Glu Ile Leu Glu Leu  
                           50                      55                      60  
 gcc ggc aat gcc gcg agg gac aac aag aag gcc cgg ata gcc ccg aga 419  
 Ala Gly Asn Ala Ala Arg Asp Asn Lys Lys Ala Arg Ile Ala Pro Arg  
                           65                      70                      75  
 cac atc ttg ctg gca gtt gcc aat gac gag gag ctc aac cag ctg cta 467  
 His Ile Leu Leu Ala Val Ala Asn Asp Glu Glu Leu Asn Gln Leu Leu  
                           80                      85                      90                      95  
 aaa gga gtg acc atc gcc agt gga ggc gtc ctg ccc aga att cac ccc 515  
 Lys Gly Val Thr Ile Ala Ser Gly Gly Val Leu Pro Arg Ile His Pro  
                           100                      105                      110  
 gaa ctg ctg gcc aaa aag cga ggg acc aaa ggc aag tcg gaa acg atc 563  
 Glu Leu Leu Ala Lys Lys Arg Gly Thr Lys Gly Lys Ser Glu Thr Ile  
                           115                      120                      125  
 ctc tcc cca ccc cca gag aaa aga ggc agg aag gcc acg tca ggc aag 611

Leu	Ser	Pro	Pro	Pro	Glu	Lys	Arg	Gly	Arg	Lys	Ala	Thr	Ser	Gly	Lys		
		130					135					140					
aag	ggg	ggg	aag	aaa	tcc	aag	gct	gcc	aaa	cca	cgg	acg	tcc	aaa	aag	659	
Lys	Gly	Gly	Lys	Lys	Ser	Lys	Ala	Ala	Lys	Pro	Arg	Thr	Ser	Lys	Lys		
	145					150				155							
tcc	aaa	cca	aag	gac	agc	gat	aaa	gaa	gga	act	tca	aat	tcc	acc	tct	707	
Ser	Lys	Pro	Lys	Asp	Ser	Asp	Lys	Glu	Gly	Thr	Ser	Asn	Ser	Thr	Ser		
160					165					170					175		
gaa	gat	ggg	cca	ggg	gat	gga	ttc	acc	att	ctg	tct	tct	aag	agc	ctt	755	
Glu	Asp	Gly	Pro	Gly	Asp	Gly	Phe	Thr	Ile	Leu	Ser	Ser	Lys	Ser	Leu		
				180					185					190			
gtt	ctg	gga	cag	aag	ctg	tcc	tta	acc	cag	agt	gac	atc	agc	cat	att	803	
Val	Leu	Gly	Gln	Lys	Leu	Ser	Leu	Thr	Gln	Ser	Asp	Ile	Ser	His	Ile		
			195					200					205				
ggc	tcc	atg	aga	gtg	gag	ggc	att	gtc	cac	cca	acc	aca	gcc	gaa	att	851	
Gly	Ser	Met	Arg	Val	Glu	Gly	Ile	Val	His	Pro	Thr	Thr	Ala	Glu	Ile		
		210					215					220					
gac	ctc	aaa	gaa	gat	ata	ggt	aaa	gcc	ttg	gaa	aag	gct	ggg	gga	aaa	899	
Asp	Leu	Lys	Glu	Asp	Ile	Gly	Lys	Ala	Leu	Glu	Lys	Ala	Gly	Gly	Lys		
	225					230					235						
gag	ttc	ttg	gaa	acg	gta	aag	gag	ctt	cgc	aaa	tcc	caa	ggc	cct	ttg	947	
Glu	Phe	Leu	Glu	Thr	Val	Lys	Glu	Leu	Arg	Lys	Ser	Gln	Gly	Pro	Leu		
240					245				250						255		
gaa	gtc	gcc	gaa	gcc	gcc	gtc	agc	caa	tcc	agt	gga	ctc	gca	gcc	aaa	995	
Glu	Val	Ala	Glu	Ala	Ala	Val	Ser	Gln	Ser	Ser	Gly	Leu	Ala	Ala	Lys		
				260					265					270			
ttt	gtc	atc	cac	tgt	cac	atc	cct	cag	tgg	ggc	tcc	gac	aaa	tgt	gaa	1043	
Phe	Val	Ile	His	Cys	His	Ile	Pro	Gln	Trp	Gly	Ser	Asp	Lys	Cys	Glu		
			275					280					285				
gaa	cag	ctt	gaa	gag	acc	atc	aaa	aac	tgc	ctg	tca	gcg	gcg	gag	gac	1091	
Glu	Gln	Leu	Glu	Glu	Thr	Ile	Lys	Asn	Cys	Leu	Ser	Ala	Ala	Glu	Asp		
		290					295					300					
aag	aag	cta	aag	tcc	gtc	gcg	ttc	ccg	cct	ttc	ccc	agc	ggc	aga	aac	1139	
Lys	Lys	Leu	Lys	Ser	Val	Ala	Phe	Pro	Pro	Phe	Pro	Ser	Gly	Arg	Asn		
	305					310					315						
tgc	ttt	ccc	aaa	cag	act	gcg	gcc	cag	gtg	acc	ctc	aaa	gcc	atc	tca	1187	
Cys	Phe	Pro	Lys	Gln	Thr	Ala	Ala	Gln	Val	Thr	Leu	Lys	Ala	Ile	Ser		
320					325					330					335		
gcc	cac	ttt	gat	gac	tcg	agc	gcg	tcc	tcg	ctg	aag	aac	gtg	tac	ttc	1235	
Ala	His	Phe	Asp	Asp	Ser	Ser	Ala	Ser	Ser	Leu	Lys	Asn	Val	Tyr	Phe		
				340					345					350			
ctg	ctc	ttc	gac	agc	gag	agc	atc	ggc	atc	tac	gtg	cag	gag	atg	gcc	1283	
Leu	Leu	Phe	Asp	Ser	Glu	Ser	Ile	Gly	Ile	Tyr	Val	Gln	Glu	Met	Ala		

355

360

365

aag ctc gac gcc aag tag ccgccgcaact ttccagcagg gatcggagga 1331  
Lys Leu Asp Ala Lys  
370

cgacccgagt cccaagagtg gggtttttgct ttttaaaagg agagaggagg ggtgatggca 1391  
ggggagtgga ggggtggccgg gcaggtcctg ccggcgagcagg gagccctctg cccttcacac 1451  
tctcctccaa aagagcctcc atctgtaagg aagcaggtct ccgcgagggg tttctttcca 1511  
tgtgttttcc tcctgttggt ttagaacttt tttaaaaaaa cagacctcgt tttagattta 1571  
tagcattgac ttttacacac attcacacaa gaaaaaaatc ctttcaaat tcttaaattct 1631  
tctgttcctc ctttttccaa gggaagaggg caaaaagtgg cctgggctct gttggtgtgc 1691  
gtgttccgtg gcggagagaa gaaaatggga aagacatctc 1731

<210> 62  
<211> 372  
<212> PRT  
<213> Homo sapiens

<400> 62  
Met Ser Gly Arg Ser Gly Lys Lys Lys Met Ser Lys Leu Ser Arg Ser  
1 5 10 15  
Ala Arg Ala Gly Val Ile Phe Pro Val Gly Arg Leu Met Arg Tyr Leu  
20 25 30  
Lys Lys Gly Thr Phe Lys Tyr Arg Ile Ser Val Gly Ala Pro Val Tyr  
35 40 45  
Met Ala Ala Val Ile Glu Tyr Leu Ala Ala Glu Ile Leu Glu Leu Ala  
50 55 60  
Gly Asn Ala Ala Arg Asp Asn Lys Lys Ala Arg Ile Ala Pro Arg His  
65 70 75 80  
Ile Leu Leu Ala Val Ala Asn Asp Glu Glu Leu Asn Gln Leu Leu Lys  
85 90 95  
Gly Val Thr Ile Ala Ser Gly Gly Val Leu Pro Arg Ile His Pro Glu  
100 105 110  
Leu Leu Ala Lys Lys Arg Gly Thr Lys Gly Lys Ser Glu Thr Ile Leu  
115 120 125  
Ser Pro Pro Pro Glu Lys Arg Gly Arg Lys Ala Thr Ser Gly Lys Lys  
130 135 140  
Gly Gly Lys Lys Ser Lys Ala Ala Lys Pro Arg Thr Ser Lys Lys Ser  
145 150 155 160  
Lys Pro Lys Asp Ser Asp Lys Glu Gly Thr Ser Asn Ser Thr Ser Glu  
165 170 175  
Asp Gly Pro Gly Asp Gly Phe Thr Ile Leu Ser Ser Lys Ser Leu Val  
180 185 190  
Leu Gly Gln Lys Leu Ser Leu Thr Gln Ser Asp Ile Ser His Ile Gly  
195 200 205  
Ser Met Arg Val Glu Gly Ile Val His Pro Thr Thr Ala Glu Ile Asp  
210 215 220  
Leu Lys Glu Asp Ile Gly Lys Ala Leu Glu Lys Ala Gly Gly Lys Glu  
225 230 235 240

Phe Leu Glu Thr Val Lys Glu Leu Arg Lys Ser Gln Gly Pro Leu Glu  
245 250 255  
Val Ala Glu Ala Ala Val Ser Gln Ser Ser Gly Leu Ala Ala Lys Phe  
260 265 270  
Val Ile His Cys His Ile Pro Gln Trp Gly Ser Asp Lys Cys Glu Glu  
275 280 285  
Gln Leu Glu Glu Thr Ile Lys Asn Cys Leu Ser Ala Ala Glu Asp Lys  
290 295 300  
Lys Leu Lys Ser Val Ala Phe Pro Pro Phe Pro Ser Gly Arg Asn Cys  
305 310 315 320  
Phe Pro Lys Gln Thr Ala Ala Gln Val Thr Leu Lys Ala Ile Ser Ala  
325 330 335  
His Phe Asp Asp Ser Ser Ala Ser Ser Leu Lys Asn Val Tyr Phe Leu  
340 345 350  
Leu Phe Asp Ser Glu Ser Ile Gly Ile Tyr Val Gln Glu Met Ala Lys  
355 360 365  
Leu Asp Ala Lys  
370

<210> 63  
<211> 910  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (21)..(698)

<400> 63  
aaagtaaggg tgtcgtgctg atg gcc ctg tgc gca ctg acc cgc gct ctg cgc 53  
Met Ala Leu Cys Ala Leu Thr Arg Ala Leu Arg  
1 5 10

tct ctg aac ctg gcg ccc ccg acc gtc gcc gcc cct gcc ccg agt ctg 101  
Ser Leu Asn Leu Ala Pro Pro Thr Val Ala Ala Pro Ala Pro Ser Leu  
15 20 25

ttc ccc gcc gcc cag atg atg aac aat ggc ctc ctc caa cag ccc tct 149  
Phe Pro Ala Ala Gln Met Met Asn Asn Gly Leu Leu Gln Gln Pro Ser  
30 35 40

gcc ttg atg ttg ctc ccc tgc cgc cca gtt ctt act tct gtg gcc ctt 197  
Ala Leu Met Leu Leu Pro Cys Arg Pro Val Leu Thr Ser Val Ala Leu  
45 50 55

aat gcc aac ttt gtg tcc tgg aag agt cgt acc aag tac acc att aca 245  
Asn Ala Asn Phe Val Ser Trp Lys Ser Arg Thr Lys Tyr Thr Ile Thr  
60 65 70 75

cca gtg aag atg agg aag tct ggg ggc cga gac cac aca ggc cga atc 293  
Pro Val Lys Met Arg Lys Ser Gly Gly Arg Asp His Thr Gly Arg Ile  
80 85 90

cgg gtg cat ggt att ggc ggg ggc cac aag caa cgt tat cga atg att 341  
Arg Val His Gly Ile Gly Gly Gly His Lys Gln Arg Tyr Arg Met Ile

95	100	105	
gac ttt ctg cgt ttc cgg cct gag gag acc aag tca gga ccc ttt gag			389
Asp Phe Leu Arg Phe Arg Pro Glu Glu Thr Lys Ser Gly Pro Phe Glu			
110	115	120	
gag aag gtt atc caa gtc cgc tat gat ccc tgt agg tca gca gac ata			437
Glu Lys Val Ile Gln Val Arg Tyr Asp Pro Cys Arg Ser Ala Asp Ile			
125	130	135	
gct ctg gtt gct ggg ggc agc cgg aaa cgc tgg atc atc gcc aca gaa			485
Ala Leu Val Ala Gly Gly Ser Arg Lys Arg Trp Ile Ile Ala Thr Glu			
140	145	150	155
aac atg cag gct gga gat aca atc ttg aac tct aac cac ata ggc cga			533
Asn Met Gln Ala Gly Asp Thr Ile Leu Asn Ser Asn His Ile Gly Arg			
160	165	170	
atg gca gtt gct gct cgg gaa ggg gat gcg cat cct ctt ggg gct ctg			581
Met Ala Val Ala Ala Arg Glu Gly Asp Ala His Pro Leu Gly Ala Leu			
175	180	185	
cct gtg ggg acc ctc atc aac aac gtg gaa agt gag cca ggc cgg ggt			629
Pro Val Gly Thr Leu Ile Asn Asn Val Glu Ser Glu Pro Gly Arg Gly			
190	195	200	
gcc caa tat atc cga gct gca ggt gct gga aac gtg cgt agc aac agt			677
Ala Gln Tyr Ile Arg Ala Ala Gly Ala Gly Asn Val Arg Ser Asn Ser			
205	210	215	
agg ccg agt atc caa cgt tga tcataacaaa cgggtcattg gcaaggcagg			728
Arg Pro Ser Ile Gln Arg			
220	225		
tcgcaaccgc tggctgggca agaggcctaa cagtgggcgg tggcaccgca aggggggctg			788
ggctggccga aagattcggc cactaccccc catgaagagt tacgtgaagc tgccttctgc			848
ttctgcccac agctgatata cctgtactct aataaaatgc cccccccccc cgttttaatc			908
tg			910

<210> 64  
 <211> 225  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
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 1 5 10 15  
 Pro Pro Thr Val Ala Ala Pro Ala Pro Ser Leu Phe Pro Ala Ala Gln  
 20 25 30  
 Met Met Asn Asn Gly Leu Leu Gln Gln Pro Ser Ala Leu Met Leu Leu  
 35 40 45  
 Pro Cys Arg Pro Val Leu Thr Ser Val Ala Leu Asn Ala Asn Phe Val  
 50 55 60



55                      60                      65                      70

gtg ttg gag tcc gca gag cac tcg gaa cct ccc cag gcc tcc agc agc    413  
Val Leu Glu Ser Ala Glu His Ser Glu Pro Pro Gln Ala Ser Ser Ser  
                    75                      80                      85

atg acc gcc tgt ggc ctg gct cgg gac gcc ccg agg aag cag ccc ggc    461  
Met Thr Ala Cys Gly Leu Ala Arg Asp Ala Pro Arg Lys Gln Pro Gly  
                    90                      95                      100

ggt cag tcc agc aca gcc agc gct ggg ccc ccg tcc tga cctgagcggg    510  
Gly Gln Ser Ser Thr Ala Ser Ala Gly Pro Pro Ser  
                    105                      110

taccaccagc cccaggcctg cggaggcgct agtccaccag agccccctccc cgccccctctc 570

cccactccgc atccctcgcc cccctcccca cctcccaccc cccacccctgt aaactaggcg 630

gctgcagcaa gcagaccttc gcatcaacac agcagacacc aaaaaccagt gagagccccg 690

ctctctaccg cccggcccca gcaactcgcta gctttcttga cacctggaac tgtgcacctg 750

gcaccaagcg gaaaataaac tccaagcagc cagt                                      784

<210> 66  
<211> 114  
<212> PRT  
<213> Homo sapiens

<400> 66  
Met Ala Ala Ile Pro Ser Ser Gly Ser Leu Val Ala Thr His Asp Tyr  
1                      5                      10                      15  
Tyr Arg Arg Arg Leu Gly Ser Thr Ser Ser Asn Ser Ser Cys Ser Ser  
                    20                      25                      30  
Thr Glu Cys Pro Gly Glu Ala Ile Pro His Pro Pro Gly Leu Pro Lys  
                    35                      40                      45  
Ala Asp Pro Gly His Trp Trp Ala Ser Phe Phe Phe Gly Lys Ser Thr  
                    50                      55                      60  
Leu Pro Phe Met Ala Thr Val Leu Glu Ser Ala Glu His Ser Glu Pro  
65                      70                      75                      80  
Pro Gln Ala Ser Ser Ser Met Thr Ala Cys Gly Leu Ala Arg Asp Ala  
                    85                      90                      95  
Pro Arg Lys Gln Pro Gly Gly Gln Ser Ser Thr Ala Ser Ala Gly Pro  
                    100                      105                      110  
Pro Ser

<210> 67  
<211> 984  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (348)..(770)

<400> 67  
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gtcgccggag agggagggca ccgctgtcgc cagaagccaa ggagtcctca gtgaccgtgg 180  
gatccacaac atctccacat cgctgtcccc acccagccag ggcagcgcca gcactagctc 240  
agacgcaagg acggaaccgc tggactccag gttccttgcc tgggagtagg agaaatccac 300  
ctgtggtggg ctgagtgtgg cctgagggac aggccctggg tcccggg atg ccc ctg 356  
Met Pro Leu  
1  
ccc gag ccc agc gag cag gag ggt gag agt gtg aag gcc agc cag gag 404  
Pro Glu Pro Ser Glu Gln Glu Gly Glu Ser Val Lys Ala Ser Gln Glu  
5 10 15  
cca tcc ccc aag cca ggc aca gaa gtc atc ccg gca gcc ccc agg aag 452  
Pro Ser Pro Lys Pro Gly Thr Glu Val Ile Pro Ala Ala Pro Arg Lys  
20 25 30 35  
ccc aga aag ttc tcc aaa ctg gtc ctg ctc aca gcc tcc aaa gac agc 500  
Pro Arg Lys Phe Ser Lys Leu Val Leu Leu Thr Ala Ser Lys Asp Ser  
40 45 50  
acc aag gtg gcg ggg gcc aag cgc aag ggt gtg cac tgt gtc atg tcc 548  
Thr Lys Val Ala Gly Ala Lys Arg Lys Gly Val His Cys Val Met Ser  
55 60 65  
ctg ggg gtg ccc ggc ccc gcc acc ctt gcc aag gcc ctc ctc cag acc 596  
Leu Gly Val Pro Gly Pro Ala Thr Leu Ala Lys Ala Leu Leu Gln Thr  
70 75 80  
cac ccc gag gcc cag cgg gcc att gag gca gcc cct cag gag cct gag 644  
His Pro Glu Ala Gln Arg Ala Ile Glu Ala Ala Pro Gln Glu Pro Glu  
85 90 95  
cag aaa cgg agc agg cag gac cca ggc aca gac aga aca gaa gac agt 692  
Gln Lys Arg Ser Arg Gln Asp Pro Gly Thr Asp Arg Thr Glu Asp Ser  
100 105 110 115  
gga tta gca gcg ggg cct cct gag gct gct ggg gag aac ttt gcc ccc 740  
Gly Leu Ala Ala Gly Pro Pro Glu Ala Ala Gly Glu Asn Phe Ala Pro  
120 125 130  
tgc tct gtg gcg ccc ggc aag tcc ctg taa ccttgacaac aggcgcaccc 790  
Cys Ser Val Ala Pro Gly Lys Ser Leu  
135 140  
tcccggggcca ccaaccagc cataggctct tctctgtccg cagggttct ggggccaaat 850  
gggtgaatct ttgctttcaa cattgtgtga tttcttttct tttttttttt ttttttttag 910  
atcaagtata agttactttt gtaagcagaa aaatactttc aaacaagaat aaaagaagct 970

gttcgctaga cccc

984

<210> 68  
<211> 140  
<212> PRT  
<213> Homo sapiens

<400> 68  
Met Pro Leu Pro Glu Pro Ser Glu Gln Glu Gly Glu Ser Val Lys Ala  
1 5 10 15  
Ser Gln Glu Pro Ser Pro Lys Pro Gly Thr Glu Val Ile Pro Ala Ala  
20 25 30  
Pro Arg Lys Pro Arg Lys Phe Ser Lys Leu Val Leu Leu Thr Ala Ser  
35 40 45  
Lys Asp Ser Thr Lys Val Ala Gly Ala Lys Arg Lys Gly Val His Cys  
50 55 60  
Val Met Ser Leu Gly Val Pro Gly Pro Ala Thr Leu Ala Lys Ala Leu  
65 70 75 80  
Leu Gln Thr His Pro Glu Ala Gln Arg Ala Ile Glu Ala Ala Pro Gln  
85 90 95  
Glu Pro Glu Gln Lys Arg Ser Arg Gln Asp Pro Gly Thr Asp Arg Thr  
100 105 110  
Glu Asp Ser Gly Leu Ala Ala Gly Pro Pro Glu Ala Ala Gly Glu Asn  
115 120 125  
Phe Ala Pro Cys Ser Val Ala Pro Gly Lys Ser Leu  
130 135 140

<210> 69  
<211> 864  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (357)..(614)

<400> 69  
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cctccaggaa aagctcgcg aagacgaggt tctgcggaga gagaggctcc aagcagtctg 120  
ggaagtgtag tccagttggc ttagcagtag tttcgttggg ggggagccga ggttcggga 180  
aggggctagg ccggcttgaa aagagattat gactgtacct tttactttg tagctggaac 240  
acaagaagtg tttgtttaat gaatgacgta cacatttaag atctgtttgg acgcgaggga 300  
taatcctgtg aattgctaag agttcactgg gtttggccct tagtggtgac ttcagt atg 359  
Met  
1

ctg aga cgg aaa cca aca cgc cta gag cta aag ctt gat gac att gaa 407  
Leu Arg Arg Lys Pro Thr Arg Leu Glu Leu Lys Leu Asp Asp Ile Glu

5	10	15	
gag ttt gag aac att cga aag gac ctg gag acc cgt aag aaa cag aag			455
Glu Phe Glu Asn Ile Arg Lys Asp Leu Glu Thr Arg Lys Lys Gln Lys			
20	25	30	
gaa gat gtg gaa gtt gta gga ggc agt gat gga gaa gga gcc att ggg			503
Glu Asp Val Glu Val Val Gly Gly Ser Asp Gly Glu Gly Ala Ile Gly			
35	40	45	
ctt agc agt gat ccc aag agc cgg gaa caa atg atc aat gat cgg att			551
Leu Ser Ser Asp Pro Lys Ser Arg Glu Gln Met Ile Asn Asp Arg Ile			
50	55	60	65
ggg tat aaa ccc caa ccc aag ccc aat aat cgt tca tct caa ttt gga			599
Gly Tyr Lys Pro Gln Pro Lys Pro Asn Asn Arg Ser Ser Gln Phe Gly			
70	75	80	
agt ctt gaa ttt tag agatggatta tcttgcagtc cagagcgctg gaatggaata			654
Ser Leu Glu Phe			
85			
aaatgatggc agaagtacaa accagattta gagaattgag tgcttgcagt caagcagaat			714
gtacctctctg cagagacaaa tcttctgcat gagattactg atgcttcact tgcactctaa			774
gctggaatcc aaactctggt ttgtctcttg aaaatttgac tctataaaac tgatctgatt			834
ttctgttttt aaaaataaat atatttttgg			864

<210> 70  
 <211> 85  
 <212> PRT  
 <213> Homo sapiens

<400> 70  
 Met Leu Arg Arg Lys Pro Thr Arg Leu Glu Leu Lys Leu Asp Asp Ile  
 1 5 10 15  
 Glu Glu Phe Glu Asn Ile Arg Lys Asp Leu Glu Thr Arg Lys Lys Gln  
 20 25 30  
 Lys Glu Asp Val Glu Val Val Gly Gly Ser Asp Gly Glu Gly Ala Ile  
 35 40 45  
 Gly Leu Ser Ser Asp Pro Lys Ser Arg Glu Gln Met Ile Asn Asp Arg  
 50 55 60  
 Ile Gly Tyr Lys Pro Gln Pro Lys Pro Asn Asn Arg Ser Ser Gln Phe  
 65 70 75 80  
 Gly Ser Leu Glu Phe  
 85

<210> 71  
 <211> 2617  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (121)..(1860)

<400> 71

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aggcctgcgg aggggcggtta tctggagggc cgcgggtgca ggccgcagtg acagggccgc 60

tcgccccgct agtctgcct gtctcccggg gcagctgtgt tcgcggcctg caggcccaac 120

atg gcg cag gag gtg tcg gag tac ctg agc cag aac ccg cgg gtg gca 168
Met Ala Gln Glu Val Ser Glu Tyr Leu Ser Gln Asn Pro Arg Val Ala
  1             5             10             15

gcc tgg gtg gag gcg ctg cgc tgc gac ggc gag act gac aaa cac tgg 216
Ala Trp Val Glu Ala Leu Arg Cys Asp Gly Glu Thr Asp Lys His Trp
             20             25             30

cgc cac cgc cgg gat ttt ttg ctt cgc aac gcc ggg gac ctg gcc ccc 264
Arg His Arg Arg Asp Phe Leu Leu Arg Asn Ala Gly Asp Leu Ala Pro
             35             40             45

gct ggc ggc gct gcc tcc gct agc acg gat gaa gct gcc gac gcc gag 312
Ala Gly Gly Ala Ala Ser Ala Ser Thr Asp Glu Ala Ala Asp Ala Glu
             50             55             60

agc ggg acc cga aac cgg cag ctg cag cag ctc atc tcc ttt tcc atg 360
Ser Gly Thr Arg Asn Arg Gln Leu Gln Gln Leu Ile Ser Phe Ser Met
             65             70             75             80

gcc tgg gcg aac cac gtc ttc ctc ggg tgc cga tac cct caa aaa gtt 408
Ala Trp Ala Asn His Val Phe Leu Gly Cys Arg Tyr Pro Gln Lys Val
             85             90             95

atg gat aaa ata ctt agt atg gct gaa ggc atc aaa gtg aca gat gct 456
Met Asp Lys Ile Leu Ser Met Ala Glu Gly Ile Lys Val Thr Asp Ala
             100            105            110

cca acc tat aca aca aga gat gaa ctg gtt gcc aag gtg aag aaa aga 504
Pro Thr Tyr Thr Thr Arg Asp Glu Leu Val Ala Lys Val Lys Lys Arg
             115            120            125

ggg ata tcg agt agc aat gaa ggg gta gaa gag cca tcc aaa aaa cga 552
Gly Ile Ser Ser Ser Asn Glu Gly Val Glu Glu Pro Ser Lys Lys Arg
             130            135            140

gtt ata gaa gga aaa aac agt tct gca gtt gag caa gat cac gca aaa 600
Val Ile Glu Gly Lys Asn Ser Ser Ala Val Glu Gln Asp His Ala Lys
             145            150            155            160

acc tct gcc aag aca gaa cgt gca tca gct cag cag gaa aac agt tca 648
Thr Ser Ala Lys Thr Glu Arg Ala Ser Ala Gln Gln Glu Asn Ser Ser
             165            170            175

acg tgt ata ggg tcg gcc atc aaa tca gag agt ggg aac tca gct cgg 696
Thr Cys Ile Gly Ser Ala Ile Lys Ser Glu Ser Gly Asn Ser Ala Arg
             180            185            190

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agc Ser	tct Ser	ggc Gly 195	atc Ile	tcc Ser	agt Ser	cag Gln	aat Asn 200	agc Ser	tct Ser	aca Thr	agt Ser	gat Asp 205	gga Gly	gat Asp	cga Arg	744
tct Ser	gtt Val 210	tcc Ser	agc Ser	caa Gln	agc Ser	agc Ser	agc Ser	agc Ser	gtt Val	tcc Ser	tct Ser	cag Gln 220	gta Val	aca Thr	acg Thr	792
gca Ala 225	gga Gly	tct Ser	ggg Gly	aaa Lys 230	gct Ala	tct Ser	gaa Glu	gca Ala	gaa Glu	gct Ala 235	cca Pro	gat Asp	aaa Lys	cac His	ggt Gly 240	840
tca Ser	tca Ser	ttt Phe	gtt Val	tcc Ser 245	ttg Leu	ctg Leu	aaa Lys	tcc Ser	agt Ser 250	gtg Val	aat Asn	agt Ser	cac His	atg Met 255	acc Thr	888
caa Gln	tcc Ser	act Thr 260	gat Asp	tct Ser	aga Arg	caa Gln	caa Gln 265	agt Ser	gga Gly	tca Ser	cct Pro	aaa Lys 270	aag Lys	agt Ser	gct Ala	936
ttg Leu	gaa Glu 275	ggc Gly	tct Ser	tca Ser	gcc Ala	tca Ser	gct Ala 280	tct Ser	cga Arg	agc Ser	agc Ser	tca Ser 285	gag Glu	atc Ile	gag Glu	984
gtg Val 290	ccc Pro	ttg Leu	ttg Leu	ggc Gly	tcc Ser	tca Ser 295	gga Gly	agc Ser	tca Ser	gag Glu	gta Val 300	gaa Glu	ttg Leu	cca Pro	cta Leu	1032
ttg Leu 305	tct Ser	tcc Ser	aaa Lys	cct Pro	agt Ser	tca Ser	gag Glu	aca Thr	gct Ala	tca Ser 315	agt Ser	ggg Gly	tta Leu	act Thr	tcc Ser 320	1080
aaa Lys	act Thr	agt Ser	tca Ser	gag Glu 325	gca Ala	agt Ser	gtt Val	tca Ser	tca Ser	tca Ser 330	gtt Val	gct Ala	aaa Lys	aac Asn 335	agt Ser	1128
tcc Ser	tca Ser	tca Ser	ggc Gly 340	aca Thr	tcc Ser	tta Leu	ctg Leu	act Thr 345	ccc Pro	aag Lys	agc Ser	agc Ser	tct Ser 350	tca Ser	aca Thr	1176
aat Asn	aca Thr 355	tcg Ser	ctg Leu	cta Leu	act Thr	tcc Ser	aag Lys 360	agc Ser	act Thr	tcc Ser	cag Gln	gta Val 365	gct Ala	gca Ala	tca Ser	1224
cta Leu 370	cta Leu	gct Ala	tcc Ser	aag Lys	agc Ser	agc Ser	tcc Ser	cag Gln	acc Thr	agt Ser	gga Gly 380	tct Ser	ctg Leu	gtt Val	tcc Ser	1272
aaa Lys 385	agc Ser	act Thr	tcc Ser	tta Leu	gca Ala	agt Ser	gtg Val	tcc Ser	cag Gln	ttg Leu 395	gct Ala	tct Ser	aag Lys	agt Ser	agt Ser 400	1320
tct Ser	cag Gln	act Thr	agc Ser	acc Thr 405	tca Ser	cag Gln	ttg Leu	cct Pro	tct Ser	aaa Lys 410	agt Ser	act Thr	tca Ser	cag Gln	tca Ser 415	1368
agt Ser	gag Ser	agt Ser	tct Ser	gtc Ser	aaa Ser	ttc Ser	tct Ser	tgc Ser	aag Ser	tta Ser	acc Ser	aat Ser	gaa Ser	gat Ser	gtg Ser	1416

Ser	Glu	Ser	Ser	Val	Lys	Phe	Ser	Cys	Lys	Leu	Thr	Asn	Glu	Asp	Val	
			420					425					430			
aaa	cag	aag	caa	cct	ttt	ttc	aat	aga	cta	tat	aaa	acg	gtg	gca	tgg	1464
Lys	Gln	Lys	Gln	Pro	Phe	Phe	Asn	Arg	Leu	Tyr	Lys	Thr	Val	Ala	Trp	
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aag	ttg	gta	gct	gtt	ggc	ttt	agt	ccc	aat	gtg	aat	cat	gga	gag		1512
Lys	Leu	Val	Ala	Val	Gly	Gly	Phe	Ser	Pro	Asn	Val	Asn	His	Gly	Glu	
		450				455					460					
ctc	cta	aat	gca	gct	att	gag	gct	ctg	aaa	gca	aca	ctg	gat	gta	ttt	1560
Leu	Leu	Asn	Ala	Ala	Ile	Glu	Ala	Leu	Lys	Ala	Thr	Leu	Asp	Val	Phe	
465					470					475					480	
ttt	gtc	cca	cta	aaa	gaa	ttg	gca	gat	ctg	cct	caa	aat	aag	agc	tct	1608
Phe	Val	Pro	Leu	Lys	Glu	Leu	Ala	Asp	Leu	Pro	Gln	Asn	Lys	Ser	Ser	
				485					490					495		
caa	gaa	agt	att	gtt	tgt	gaa	ttg	agg	tgc	aag	tct	gtg	tat	ttg	ggc	1656
Gln	Glu	Ser	Ile	Val	Cys	Glu	Leu	Arg	Cys	Lys	Ser	Val	Tyr	Leu	Gly	
			500					505					510			
act	ggc	tgt	gga	aaa	agc	aaa	gaa	aat	gca	aaa	gca	gtt	gca	tca	aga	1704
Thr	Gly	Cys	Gly	Lys	Ser	Lys	Glu	Asn	Ala	Lys	Ala	Val	Ala	Ser	Arg	
		515					520					525				
gaa	gca	ttg	aag	tta	ttt	ctc	aag	aaa	aag	gtg	gtg	gta	aaa	ata	tgt	1752
Glu	Ala	Leu	Lys	Leu	Phe	Leu	Lys	Lys	Lys	Val	Val	Val	Lys	Ile	Cys	
		530				535					540					
aaa	agg	aaa	tac	aga	ggc	agt	gaa	ata	gaa	gat	cta	gta	ctc	ctt	gat	1800
Lys	Arg	Lys	Tyr	Arg	Gly	Ser	Glu	Ile	Glu	Asp	Leu	Val	Leu	Leu	Asp	
545					550					555					560	
gaa	gaa	tcg	agg	cct	gta	aac	tta	cct	cca	gca	cta	aaa	cat	cct	caa	1848
Glu	Glu	Ser	Arg	Pro	Val	Asn	Leu	Pro	Pro	Ala	Leu	Lys	His	Pro	Gln	
				565					570					575		
gaa	tta	cta	taa	tgtgtccaaa	atatcactgc	atacaatatc	tggtatttga									1900
Glu	Leu	Leu														
agagaaaaac	tgactttt	gt	atagtataaa	acacaggc	tt	tcacaaat	tt	tgtattg	c	tt						1960
tttttccagt	tttgcagaaa	atttacatt	c	tagttctct	t	cacacagtag	cagttg	taaa								2020
taatttatga	atgacagtac	acattaaa	ag	gtatgc	atta	gcagcatatt	agtatg	ctgt								2080
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gttcggtaga	gtcctaaaa	ttttgtact	a	ctttca	at	ggtgaaa	atg	tatta	ag	ttg						2200
tctaccatgt	tttctttt	ct	agctga	ataa	accacat	caa	aggaa	aggga	ccacag	tatt						2260
tgaatgtttg	aaagtctgta	aagctta	agg	ttttaaaa	at	gttgccc	gta	atgttga	acg							2320
tgtctgttaa	aaaataaa	ag	aaaaa	atag	t	gcttca	aac	tattttt	atg	aga	ag	ttg	ta			2380

agcatttttt agatataaag cagtataaag tacttggttat tttactctga agttgttttaa 2440  
aattcaccat gactttgacc gctgaagatt ctttaagcgg gttaatttat gttttgaggt 2500  
ggaatacaat ttacactttt ttcttaaaaa catgaatgtg ggtttctata ttaagcatat 2560  
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<210> 72  
<211> 579  
<212> PRT  
<213> Homo sapiens

<400> 72  
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Ala Trp Val Glu Ala Leu Arg Cys Asp Gly Glu Thr Asp Lys His Trp  
20 25 30  
Arg His Arg Arg Asp Phe Leu Leu Arg Asn Ala Gly Asp Leu Ala Pro  
35 40 45  
Ala Gly Gly Ala Ala Ser Ala Ser Thr Asp Glu Ala Ala Asp Ala Glu  
50 55 60  
Ser Gly Thr Arg Asn Arg Gln Leu Gln Gln Leu Ile Ser Phe Ser Met  
65 70 75 80  
Ala Trp Ala Asn His Val Phe Leu Gly Cys Arg Tyr Pro Gln Lys Val  
85 90 95  
Met Asp Lys Ile Leu Ser Met Ala Glu Gly Ile Lys Val Thr Asp Ala  
100 105 110  
Pro Thr Tyr Thr Thr Arg Asp Glu Leu Val Ala Lys Val Lys Lys Arg  
115 120 125  
Gly Ile Ser Ser Ser Asn Glu Gly Val Glu Glu Pro Ser Lys Lys Arg  
130 135 140  
Val Ile Glu Gly Lys Asn Ser Ser Ala Val Glu Gln Asp His Ala Lys  
145 150 155 160  
Thr Ser Ala Lys Thr Glu Arg Ala Ser Ala Gln Gln Glu Asn Ser Ser  
165 170 175  
Thr Cys Ile Gly Ser Ala Ile Lys Ser Glu Ser Gly Asn Ser Ala Arg  
180 185 190  
Ser Ser Gly Ile Ser Ser Gln Asn Ser Ser Thr Ser Asp Gly Asp Arg  
195 200 205  
Ser Val Ser Ser Gln Ser Ser Ser Ser Val Ser Ser Gln Val Thr Thr  
210 215 220  
Ala Gly Ser Gly Lys Ala Ser Glu Ala Glu Ala Pro Asp Lys His Gly  
225 230 235 240  
Ser Ser Phe Val Ser Leu Leu Lys Ser Ser Val Asn Ser His Met Thr  
245 250 255  
Gln Ser Thr Asp Ser Arg Gln Gln Ser Gly Ser Pro Lys Lys Ser Ala  
260 265 270  
Leu Glu Gly Ser Ser Ala Ser Ala Ser Arg Ser Ser Ser Glu Ile Glu  
275 280 285  
Val Pro Leu Leu Gly Ser Ser Gly Ser Ser Glu Val Glu Leu Pro Leu  
290 295 300  
Leu Ser Ser Lys Pro Ser Ser Glu Thr Ala Ser Ser Gly Leu Thr Ser  
305 310 315 320  
Lys Thr Ser Ser Glu Ala Ser Val Ser Ser Ser Val Ala Lys Asn Ser

				325					330					335					
Ser	Ser	Ser	Gly	Thr	Ser	Leu	Leu	Thr	Pro	Lys	Ser	Ser	Ser	Ser	Thr				
			340					345					350						
Asn	Thr	Ser	Leu	Leu	Thr	Ser	Lys	Ser	Thr	Ser	Gln	Val	Ala	Ala	Ser				
		355					360					365							
Leu	Leu	Ala	Ser	Lys	Ser	Ser	Ser	Gln	Thr	Ser	Gly	Ser	Leu	Val	Ser				
	370					375					380								
Lys	Ser	Thr	Ser	Leu	Ala	Ser	Val	Ser	Gln	Leu	Ala	Ser	Lys	Ser	Ser				
385					390					395					400				
Ser	Gln	Thr	Ser	Thr	Ser	Gln	Leu	Pro	Ser	Lys	Ser	Thr	Ser	Gln	Ser				
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Ser	Glu	Ser	Ser	Val	Lys	Phe	Ser	Cys	Lys	Leu	Thr	Asn	Glu	Asp	Val				
		420					425						430						
Lys	Gln	Lys	Gln	Pro	Phe	Phe	Asn	Arg	Leu	Tyr	Lys	Thr	Val	Ala	Trp				
	435						440						445						
Lys	Leu	Val	Ala	Val	Gly	Gly	Phe	Ser	Pro	Asn	Val	Asn	His	Gly	Glu				
	450				455						460								
Leu	Leu	Asn	Ala	Ala	Ile	Glu	Ala	Leu	Lys	Ala	Thr	Leu	Asp	Val	Phe				
465					470					475					480				
Phe	Val	Pro	Leu	Lys	Glu	Leu	Ala	Asp	Leu	Pro	Gln	Asn	Lys	Ser	Ser				
			485					490						495					
Gln	Glu	Ser	Ile	Val	Cys	Glu	Leu	Arg	Cys	Lys	Ser	Val	Tyr	Leu	Gly				
			500					505					510						
Thr	Gly	Cys	Gly	Lys	Ser	Lys	Glu	Asn	Ala	Lys	Ala	Val	Ala	Ser	Arg				
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Glu	Ala	Leu	Lys	Leu	Phe	Leu	Lys	Lys	Lys	Val	Val	Val	Lys	Ile	Cys				
	530				535							540							
Lys	Arg	Lys	Tyr	Arg	Gly	Ser	Glu	Ile	Glu	Asp	Leu	Val	Leu	Leu	Asp				
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<210> 73  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (39)..(1121)

<400> 73  
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cgc agc cga cgg ctg gga ggc cta agg ccc gaa tcc ccc gag agc ctc 104  
 Arg Ser Arg Arg Leu Gly Gly Leu Arg Pro Glu Ser Pro Glu Ser Leu  
 10 15 20

acc tca gtt tcg cgg acg aga cgg gcc ctt gtg gag ttc gag tcg aac 152  
 Thr Ser Val Ser Arg Thr Arg Arg Ala Leu Val Glu Phe Glu Ser Asn  
 25 30 35

cca gaa gaa acg agg gag ccc ggg tct cct ccg agt gtg cag cgg gct	200
Pro Glu Glu Thr Arg Glu Pro Gly Ser Pro Pro Ser Val Gln Arg Ala	
40 45 50	
ggc ctg ggg tcc ccc gaa agg ccg ccg aag aca agc cca gga tca ccc	248
Gly Leu Gly Ser Pro Glu Arg Pro Pro Lys Thr Ser Pro Gly Ser Pro	
55 60 65 70	
cgt ctg cag cag ggt gca ggc ttg gag tca ccc caa ggg cag cca gag	296
Arg Leu Gln Gln Gly Ala Gly Leu Glu Ser Pro Gln Gly Gln Pro Glu	
75 80 85	
cca ggc gca gcg tcc ccc cag cgt cag caa gac cta cac ctg gag tcg	344
Pro Gly Ala Ala Ser Pro Gln Arg Gln Gln Asp Leu His Leu Glu Ser	
90 95 100	
cct caa aga cag cca gag tac agt cct gaa tcc cca cga tgt cag ccg	392
Pro Gln Arg Gln Pro Glu Tyr Ser Pro Glu Ser Pro Arg Cys Gln Pro	
105 110 115	
aag cca agt gag gag gca cca aag tgt tct cag gac cag gga gta ctg	440
Lys Pro Ser Glu Glu Ala Pro Lys Cys Ser Gln Asp Gln Gly Val Leu	
120 125 130	
gcc tcg gag ttg gcc cag aat aag gag gag ctg acc ccg ggg gcc ccc	488
Ala Ser Glu Leu Ala Gln Asn Lys Glu Glu Leu Thr Pro Gly Ala Pro	
135 140 145 150	
cag cat cag cta ccg ccg gtc cca gga tca cca gag cct tac ccc ggt	536
Gln His Gln Leu Pro Pro Val Pro Gly Ser Pro Glu Pro Tyr Pro Gly	
155 160 165	
cag caa gct ccc ggt ccg gag ccc tct cag cca cta ctg gag ctg aca	584
Gln Gln Ala Pro Gly Pro Glu Pro Ser Gln Pro Leu Leu Glu Leu Thr	
170 175 180	
ccc agg gca cct ggc tcc ccc ccg ggt cag cat gag ccg agc aag cca	632
Pro Arg Ala Pro Gly Ser Pro Arg Gly Gln His Glu Pro Ser Lys Pro	
185 190 195	
cct cca gct ggg gag acg gtg aca ggc ggc ttc ggg gca aag aag cga	680
Pro Pro Ala Gly Glu Thr Val Thr Gly Gly Phe Gly Ala Lys Lys Arg	
200 205 210	
aaa ggt tct tca tcc cag gcc cca gcg tcc aag aag ttg aat aaa gag	728
Lys Gly Ser Ser Ser Gln Ala Pro Ala Ser Lys Lys Leu Asn Lys Glu	
215 220 225 230	
gag ctt cct gta atc ccg aag ggg aag ccc aaa tcg ggg cga gtg tgg	776
Glu Leu Pro Val Ile Pro Lys Gly Lys Pro Lys Ser Gly Arg Val Trp	
235 240 245	
aag gac cgc tcc aag aaa aga ttc tcc cag atg ctt cag gac aag ccc	824
Lys Asp Arg Ser Lys Lys Arg Phe Ser Gln Met Leu Gln Asp Lys Pro	
250 255 260	
ctg cgc aca tcg tgg cag ccg aag atg aag gaa cga cag gag agg aag	872

Leu Arg Thr Ser Trp Gln Arg Lys Met Lys Glu Arg Gln Glu Arg Lys  
 265 270 275  
 ctg gcc aag gac ttt gcc cgt cac ctg gag gag gag aag gag agg cgc 920  
 Leu Ala Lys Asp Phe Ala Arg His Leu Glu Glu Glu Lys Glu Arg Arg  
 280 285 290  
 cgc cag gag aag aaa cag cgc cgg gct gag aac ctg aaa cgc cgc ctg 968  
 Arg Gln Glu Lys Lys Gln Arg Arg Ala Glu Asn Leu Lys Arg Arg Leu  
 295 300 305 310  
 gag aat gag cgg aag gca gag gtc gtc caa gtg atc cga aac ccc gcc 1016  
 Glu Asn Glu Arg Lys Ala Glu Val Val Gln Val Ile Arg Asn Pro Ala  
 315 320 325  
 aag ctc aag cgg gca aag aag aag cag ctg cgc tcc att gag aag cgg 1064  
 Lys Leu Lys Arg Ala Lys Lys Lys Gln Leu Arg Ser Ile Glu Lys Arg  
 330 335 340  
 gac acc ctg gcc ctg ctg cag aag cag ccg ccc cag cag ccg gca gcc 1112  
 Asp Thr Leu Ala Leu Leu Gln Lys Gln Pro Pro Gln Gln Pro Ala Ala  
 345 350 355  
 aag atc tga gctcaggacg gcccagggcc ttccatggcc aacaaccatg 1161  
 Lys Ile  
 360  
 tcagacacag cacctcaggc cgctgctcag atgcctctgc tggagctggc actccaaacc 1221  
 catggctcca gaacagggac cccaccccg accggggctc ctcagccttt gaaggcttcc 1281  
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 gccccagaga atctaactca tgctgtcca gtctacagca aaaatattta ttgagtgcct 1761  
 gttgcataca ggcacaatcc taggcactgg caaatacaga caatagacc 1810  
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 <212> PRT  
 <213> Homo sapiens  
 <400> 74  
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			20					25					30		
Val	Glu	Phe	Glu	Ser	Asn	Pro	Glu	Glu	Thr	Arg	Glu	Pro	Gly	Ser	Pro
		35					40					45			
Pro	Ser	Val	Gln	Arg	Ala	Gly	Leu	Gly	Ser	Pro	Glu	Arg	Pro	Pro	Lys
		50				55					60				
Thr	Ser	Pro	Gly	Ser	Pro	Arg	Leu	Gln	Gln	Gly	Ala	Gly	Leu	Glu	Ser
					70					75					80
Pro	Gln	Gly	Gln	Pro	Glu	Pro	Gly	Ala	Ala	Ser	Pro	Gln	Arg	Gln	Gln
				85					90					95	
Asp	Leu	His	Leu	Glu	Ser	Pro	Gln	Arg	Gln	Pro	Glu	Tyr	Ser	Pro	Glu
			100					105					110		
Ser	Pro	Arg	Cys	Gln	Pro	Lys	Pro	Ser	Glu	Glu	Ala	Pro	Lys	Cys	Ser
		115					120					125			
Gln	Asp	Gln	Gly	Val	Leu	Ala	Ser	Glu	Leu	Ala	Gln	Asn	Lys	Glu	Glu
	130					135					140				
Leu	Thr	Pro	Gly	Ala	Pro	Gln	His	Gln	Leu	Pro	Pro	Val	Pro	Gly	Ser
	145				150					155					160
Pro	Glu	Pro	Tyr	Pro	Gly	Gln	Gln	Ala	Pro	Gly	Pro	Glu	Pro	Ser	Gln
			165					170						175	
Pro	Leu	Leu	Glu	Leu	Thr	Pro	Arg	Ala	Pro	Gly	Ser	Pro	Arg	Gly	Gln
			180					185					190		
His	Glu	Pro	Ser	Lys	Pro	Pro	Pro	Ala	Gly	Glu	Thr	Val	Thr	Gly	Gly
		195					200					205			
Phe	Gly	Ala	Lys	Lys	Arg	Lys	Gly	Ser	Ser	Ser	Gln	Ala	Pro	Ala	Ser
	210					215					220				
Lys	Lys	Leu	Asn	Lys	Glu	Glu	Leu	Pro	Val	Ile	Pro	Lys	Gly	Lys	Pro
	225				230					235					240
Lys	Ser	Gly	Arg	Val	Trp	Lys	Asp	Arg	Ser	Lys	Lys	Arg	Phe	Ser	Gln
			245					250						255	
Met	Leu	Gln	Asp	Lys	Pro	Leu	Arg	Thr	Ser	Trp	Gln	Arg	Lys	Met	Lys
			260					265					270		
Glu	Arg	Gln	Glu	Arg	Lys	Leu	Ala	Lys	Asp	Phe	Ala	Arg	His	Leu	Glu
		275					280					285			
Glu	Glu	Lys	Glu	Arg	Arg	Arg	Gln	Glu	Lys	Lys	Gln	Arg	Arg	Ala	Glu
	290					295					300				
Asn	Leu	Lys	Arg	Arg	Leu	Glu	Asn	Glu	Arg	Lys	Ala	Glu	Val	Val	Gln
	305				310					315					320
Val	Ile	Arg	Asn	Pro	Ala	Lys	Leu	Lys	Arg	Ala	Lys	Lys	Lys	Gln	Leu
			325						330					335	
Arg	Ser	Ile	Glu	Lys	Arg	Asp	Thr	Leu	Ala	Leu	Leu	Gln	Lys	Gln	Pro
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Pro	Gln	Gln	Pro	Ala	Ala	Lys	Ile								
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<210> 75
<211> 1620
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (217) .. (597)
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<400> 75



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acggaagcta cagtgagaac atagccagtc ccaaagacaa tttcaaagaa aaatgacagt 1277  
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<211> 126  
<212> PRT  
<213> Homo sapiens

<400> 76  
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20 25 30  
Ser Gly Gly Gly Gly Pro Ile Asn Pro Ala Ser Leu Pro Pro Gly Asp  
35 40 45  
Pro Gln Leu Ile Ala Leu Ile Val Glu Gln Leu Lys Ser Arg Gly Leu  
50 55 60  
Phe Asp Ser Phe Arg Arg Asp Cys Leu Ala Asp Val Asp Thr Lys Pro  
65 70 75 80  
Ala Tyr Gln Asn Leu Arg Gln Lys Val Asp Asn Phe Val Ser Thr His  
85 90 95  
Leu Asp Lys Gln Glu Trp Asn Pro Thr Met Asn Lys Asn Gln Leu Arg  
100 105 110  
Asn Gly Leu Arg Gln Ser Val Val Gln Leu Gly Asp Cys Gly  
115 120 125

<210> 77  
<211> 1349  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (185)..(1042)

<400> 77  
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gcagaggggtt aacctgggtc aaatgcacgg attctcacct cgtacagtta cgctctcccg 120

cggcacgtcc gcgaggactt gaagtcctga gcgctcaagt ttgtccgtag gtcgagagaa 180

ggcc atg gag gtg ccg cca ccg gca ccg cgg agc ttt ctc tgt aga gca 229  
Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala  
1 5 10 15

ttg tgc cta ttt ccc cga gtc ttt gct gcc gaa gct gtg act gcc gat 277  
Leu Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala Asp  
20 25 30

tcg gaa gtc ctt gag gag cgt cag aag cgg ctt ccc tac gtc cca gag 325  
Ser Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val Pro Glu  
35 40 45

ccc tat tac ccg gaa tct gga tgg gac cgc ctc cgg gag ctg ttt ggc 373  
Pro Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu Leu Phe Gly  
50 55 60

aaa gat gaa cag cag aga att tca aag gac ctt gct aat atc tgt aag 421  
Lys Asp Glu Gln Gln Arg Ile Ser Lys Asp Leu Ala Asn Ile Cys Lys  
65 70 75

acg gca gct aca gca ggc atc att ggc tgg gtg tat ggg gga ata cca 469  
Thr Ala Ala Thr Ala Gly Ile Ile Gly Trp Val Tyr Gly Gly Ile Pro  
80 85 90 95

gct ttt att cat gct aaa caa caa tac att gag cag agc cag gca gaa 517  
Ala Phe Ile His Ala Lys Gln Gln Tyr Ile Glu Gln Ser Gln Ala Glu  
100 105 110

att tat cat aac cgg ttt gat gct gtg caa tct gca cat cgt gct gcc 565  
Ile Tyr His Asn Arg Phe Asp Ala Val Gln Ser Ala His Arg Ala Ala  
115 120 125

aca cga ggc ttc att cgt tat ggc tgg cgc tgg ggt tgg aga act gca 613  
Thr Arg Gly Phe Ile Arg Tyr Gly Trp Arg Trp Gly Trp Arg Thr Ala  
130 135 140

gtg ttt gtg act ata ttc aac aca gtg aac act agt ctg aat gta tac 661  
Val Phe Val Thr Ile Phe Asn Thr Val Asn Thr Ser Leu Asn Val Tyr  
145 150 155

cga aat aaa gat gcc tta agc cat ttt gta att gca gga gct gtc acg 709  
Arg Asn Lys Asp Ala Leu Ser His Phe Val Ile Ala Gly Ala Val Thr  
160 165 170 175

gga agt ctt ttt agg ata aac gta ggc ctg cgt ggc ctg gtg gct ggt 757  
Gly Ser Leu Phe Arg Ile Asn Val Gly Leu Arg Gly Leu Val Ala Gly  
180 185 190

ggc ata att gga gcc ttg ctg ggc act cct gta gga ggc ctg ctg atg 805  
Gly Ile Ile Gly Ala Leu Leu Gly Thr Pro Val Gly Gly Leu Leu Met  
195 200 205

gca ttt cag aag tac tct ggt gag act gtt cag gaa aga aaa cag aag 853

Ala Phe Gln Lys Tyr Ser Gly Glu Thr Val Gln Glu Arg Lys Gln Lys  
 210 215 220

gat cga aag gca ctc cat gag cta aaa ctg gaa gag tgg aaa ggc aga 901  
 Asp Arg Lys Ala Leu His Glu Leu Lys Leu Glu Glu Trp Lys Gly Arg  
 225 230 235

cta caa gtt act gag cac ctc cct gag aaa att gaa agt agt tta cag 949  
 Leu Gln Val Thr Glu His Leu Pro Glu Lys Ile Glu Ser Ser Leu Gln  
 240 245 250 255

gaa gat gaa cct gag aat gat gct aag aaa att gaa gca ctg cta aac 997  
 Glu Asp Glu Pro Glu Asn Asp Ala Lys Lys Ile Glu Ala Leu Leu Asn  
 260 265 270

ctt cct aga aac cct tca gta ata gat aaa caa gac aag gac tga 1042  
 Leu Pro Arg Asn Pro Ser Val Ile Asp Lys Gln Asp Lys Asp  
 275 280 285

aagtgcctctg aacttgaaac tcaactggaga gctgaaggga gctgccatgt ccgatgaatg 1102

ccaacagaca ggccactctt tggctcagcct gctgacaaat ttaagtgcctg gtacctgtgg 1162

tggcagtggc ttgctcttgt ctttttcttt tctttttaac taagaatggg gctgttgtac 1222

tctcacttta cttatccttc aatttaaata catacttatg tttgtattaa tctatcaata 1282

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<210> 78  
 <211> 285  
 <212> PRT  
 <213> Homo sapiens

<400> 78  
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 Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala Asp Ser  
 20 25 30  
 Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val Pro Glu Pro  
 35 40 45  
 Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu Leu Phe Gly Lys  
 50 55 60  
 Asp Glu Gln Gln Arg Ile Ser Lys Asp Leu Ala Asn Ile Cys Lys Thr  
 65 70 75 80  
 Ala Ala Thr Ala Gly Ile Ile Gly Trp Val Tyr Gly Gly Ile Pro Ala  
 85 90 95  
 Phe Ile His Ala Lys Gln Gln Tyr Ile Glu Gln Ser Gln Ala Glu Ile  
 100 105 110  
 Tyr His Asn Arg Phe Asp Ala Val Gln Ser Ala His Arg Ala Ala Thr  
 115 120 125  
 Arg Gly Phe Ile Arg Tyr Gly Trp Arg Trp Gly Trp Arg Thr Ala Val  
 130 135 140  
 Phe Val Thr Ile Phe Asn Thr Val Asn Thr Ser Leu Asn Val Tyr Arg

145		150		155		160									
Asn	Lys	Asp	Ala	Leu	Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly
		165		170		175									
Ser	Leu	Phe	Arg	Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly
		180		185		190									
Ile	Ile	Gly	Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala
		195		200		205									
Phe	Gln	Lys	Tyr	Ser	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp
		210		215		220									
Arg	Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu
		225		230		235									
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Gln	Glu
				245		250								255	
Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu	Asn	Leu
		260		265		270									
Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp			
		275		280		285									

<210> 79  
 <211> 1355  
 <212> DNA  
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<220>  
 <221> CDS  
 <222> (79)..(1068)

<400> 79  
 gatggcggct tcctagttag tcggcggctg atttagaagg aggttcaggc tacggtgagc 60  
 cgaagccaca caggagcc atg gaa gtg gca gag ccc agc agc ccc act gaa 111  
                   Met Glu Val Ala Glu Pro Ser Ser Pro Thr Glu  
                   1                  5                  10  
 gag gag gag gag gaa gag gag cac tcg gca gag cct cgg ccc cgc act 159  
 Glu Glu Glu Glu Glu Glu Glu His Ser Ala Glu Pro Arg Pro Arg Thr  
                   15                  20                  25  
 cgc tcc aat cct gaa ggg gct gag gac cgg gca gta ggg gca cag gcc 207  
 Arg Ser Asn Pro Glu Gly Ala Glu Asp Arg Ala Val Gly Ala Gln Ala  
                   30                  35                  40  
 agc gtg ggc agc cgc agc gag ggt gag ggt gag gcc gcc agt gct gat 255  
 Ser Val Gly Ser Arg Ser Glu Gly Glu Gly Glu Ala Ala Ser Ala Asp  
                   45                  50                  55  
 gat ggg agc ctc aac act tca gga gcc ggc cct aag tcc tgg cag gtg 303  
 Asp Gly Ser Leu Asn Thr Ser Gly Ala Glu Pro Lys Ser Trp Gln Val  
                   60                  65                  70                  75  
 ccc ccg cca gcc cct gag gtc caa att cgg aca cca agg gtc aac tgt 351  
 Pro Pro Pro Ala Pro Glu Val Gln Ile Arg Thr Pro Arg Val Asn Cys  
                   80                  85                  90  
 cca gag aaa gtg att atc tgc ctg gac ctg tca gag gaa atg tca ctg 399

Pro	Glu	Lys	Val	Ile	Ile	Cys	Leu	Asp	Leu	Ser	Glu	Glu	Met	Ser	Leu		
			95						100			105					
cca	aag	ctg	gag	tcg	ttc	aac	ggc	tcc	aaa	acc	aac	gcc	ctc	aat	gtc	447	
Pro	Lys	Leu	Glu	Ser	Phe	Asn	Gly	Ser	Lys	Thr	Asn	Ala	Leu	Asn	Val		
			110						115			120					
tcc	cag	aag	atg	att	gag	atg	ttc	gtg	cgg	aca	aaa	cac	aag	atc	gac	495	
Ser	Gln	Lys	Met	Ile	Glu	Met	Phe	Val	Arg	Thr	Lys	His	Lys	Ile	Asp		
			125						130			135					
aaa	agc	cac	gag	ttt	gca	ctg	gtg	gtg	gtg	aac	gat	gac	acg	gcc	tgg	543	
Lys	Ser	His	Glu	Phe	Ala	Leu	Val	Val	Val	Asn	Asp	Asp	Thr	Ala	Trp		
140						145						150			155		
ctg	tct	ggc	ctg	acc	tcc	gac	ccc	cgc	gag	ctc	tgt	agc	tgc	ctc	tat	591	
Leu	Ser	Gly	Leu	Thr	Ser	Asp	Pro	Arg	Glu	Leu	Cys	Ser	Cys	Leu	Tyr		
			160						165						170		
gat	ctg	gag	acg	gcc	tcc	tgt	tcc	acc	ttc	aat	ctg	gaa	gga	ctt	ttc	639	
Asp	Leu	Glu	Thr	Ala	Ser	Cys	Ser	Thr	Phe	Asn	Leu	Glu	Gly	Leu	Phe		
			175						180			185					
agc	ctc	atc	cag	cag	aaa	act	gag	ctt	ccg	gtc	aca	gag	aac	gtg	cag	687	
Ser	Leu	Ile	Gln	Gln	Lys	Thr	Glu	Leu	Pro	Val	Thr	Glu	Asn	Val	Gln		
			190						195			200					
acg	att	ccc	ccg	cca	tat	gtg	gtc	cgc	acc	atc	ctt	gtc	tac	agc	cgt	735	
Thr	Ile	Pro	Pro	Pro	Tyr	Val	Val	Arg	Thr	Ile	Leu	Val	Tyr	Ser	Arg		
205						210						215					
cca	cct	tgc	cag	ccc	cag	ttc	tcc	ttg	acg	gag	ccc	atg	aag	aaa	atg	783	
Pro	Pro	Cys	Gln	Pro	Gln	Phe	Ser	Leu	Thr	Glu	Pro	Met	Lys	Lys	Met		
220						225						230			235		
ttc	cag	tgc	cca	tat	ttc	ttc	ttt	gac	gtt	gtt	tac	atc	cac	aat	ggc	831	
Phe	Gln	Cys	Pro	Tyr	Phe	Phe	Phe	Asp	Val	Val	Tyr	Ile	His	Asn	Gly		
			240						245						250		
act	gag	gag	aag	gag	gag	gag	atg	agt	tgg	aag	gat	atg	ttt	gcc	ttc	879	
Thr	Glu	Glu	Lys	Glu	Glu	Glu	Met	Ser	Trp	Lys	Asp	Met	Phe	Ala	Phe		
			255						260						265		
atg	ggc	agc	ctg	gat	acc	aag	ggt	acc	agc	tac	aaa	tat	gag	gtg	gca	927	
Met	Gly	Ser	Leu	Asp	Thr	Lys	Gly	Thr	Ser	Tyr	Lys	Tyr	Glu	Val	Ala		
			270			275						280					
ctg	gct	ggg	cca	gcc	ctg	gag	ttg	cac	aac	tgc	atg	gcg	aaa	ctg	ttg	975	
Leu	Ala	Gly	Pro	Ala	Leu	Glu	Leu	His	Asn	Cys	Met	Ala	Lys	Leu	Leu		
285						290						295					
gcc	cac	ccc	ctg	cag	cgg	cct	tgc	cag	agc	cat	gct	tcc	tac	agc	ctg	1023	
Ala	His	Pro	Leu	Gln	Arg	Pro	Cys	Gln	Ser	His	Ala	Ser	Tyr	Ser	Leu		
300						305						310			315		
ctg	gag	gag	gag	gat	gaa	gcc	att	gag	gtt	gag	gcc	act	gtc	tga		1068	
Leu	Glu	Glu	Glu	Asp	Glu	Ala	Ile	Glu	Val	Glu	Ala	Thr	Val				

320

325

accatccctg tacatctgca ccttcttgtg caaggaagtc cttggcctaa agccttggtt 1128  
 ctcaaactgg gttccttggg acctccggg tgggggggtt ccaggaggca cgtagggtag 1188  
 cttgcagggt cctaggaggg aaaccagga ttccaggagg gatcccagga actgtgggca 1248  
 cccattttct gtgtctccca gccatttcc actcctagtt tgtcatggat aatttttgtt 1308  
 cttccctgtg tgatttttgc catcaaaata aaaatttgag actcgtt 1355

&lt;210&gt; 80

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 80

Met Glu Val Ala Glu Pro Ser Ser Pro Thr Glu Glu Glu Glu Glu Glu  
 1 5 10 15  
 Glu Glu His Ser Ala Glu Pro Arg Pro Arg Thr Arg Ser Asn Pro Glu  
 20 25 30  
 Gly Ala Glu Asp Arg Ala Val Gly Ala Gln Ala Ser Val Gly Ser Arg  
 35 40 45  
 Ser Glu Gly Glu Gly Glu Ala Ala Ser Ala Asp Asp Gly Ser Leu Asn  
 50 55 60  
 Thr Ser Gly Ala Gly Pro Lys Ser Trp Gln Val Pro Pro Pro Ala Pro  
 65 70 75 80  
 Glu Val Gln Ile Arg Thr Pro Arg Val Asn Cys Pro Glu Lys Val Ile  
 85 90 95  
 Ile Cys Leu Asp Leu Ser Glu Glu Met Ser Leu Pro Lys Leu Glu Ser  
 100 105 110  
 Phe Asn Gly Ser Lys Thr Asn Ala Leu Asn Val Ser Gln Lys Met Ile  
 115 120 125  
 Glu Met Phe Val Arg Thr Lys His Lys Ile Asp Lys Ser His Glu Phe  
 130 135 140  
 Ala Leu Val Val Val Asn Asp Asp Thr Ala Trp Leu Ser Gly Leu Thr  
 145 150 155 160  
 Ser Asp Pro Arg Glu Leu Cys Ser Cys Leu Tyr Asp Leu Glu Thr Ala  
 165 170 175  
 Ser Cys Ser Thr Phe Asn Leu Glu Gly Leu Phe Ser Leu Ile Gln Gln  
 180 185 190  
 Lys Thr Glu Leu Pro Val Thr Glu Asn Val Gln Thr Ile Pro Pro Pro  
 195 200 205  
 Tyr Val Val Arg Thr Ile Leu Val Tyr Ser Arg Pro Pro Cys Gln Pro  
 210 215 220  
 Gln Phe Ser Leu Thr Glu Pro Met Lys Lys Met Phe Gln Cys Pro Tyr  
 225 230 235 240  
 Phe Phe Phe Asp Val Val Tyr Ile His Asn Gly Thr Glu Glu Lys Glu  
 245 250 255  
 Glu Glu Met Ser Trp Lys Asp Met Phe Ala Phe Met Gly Ser Leu Asp  
 260 265 270  
 Thr Lys Gly Thr Ser Tyr Lys Tyr Glu Val Ala Leu Ala Gly Pro Ala  
 275 280 285  
 Leu Glu Leu His Asn Cys Met Ala Lys Leu Leu Ala His Pro Leu Gln  
 290 295 300

T04269.92906950

Arg Pro Cys Gln Ser His Ala Ser Tyr Ser Leu Leu Glu Glu Glu Asp  
 305 310 315 320  
 Glu Ala Ile Glu Val Glu Ala Thr Val  
 325

<210> 81  
 <211> 1543  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (29)..(730)

<400> 81  
 gctctggggc gcgggcgatt tgtaggta atg gca ggc gtt cgg tca ctg agg 52  
 Met Ala Gly Val Arg Ser Leu Arg  
 1 5

tgt agc aga gga tgc gct ggc ggc tgt gag tgc ggc gac aag ggc aaa 100  
 Cys Ser Arg Gly Cys Ala Gly Gly Cys Glu Cys Gly Asp Lys Gly Lys  
 10 15 20

tgc agc gac tcc tcg ctg ttg ggc aag aga ctc tcc gaa gac tcg agc 148  
 Cys Ser Asp Ser Ser Leu Leu Gly Lys Arg Leu Ser Glu Asp Ser Ser  
 25 30 35 40

cgc cac cag ctg ttg cag aag tgg gcg agc atg tgg agc tcc atg agc 196  
 Arg His Gln Leu Leu Gln Lys Trp Ala Ser Met Trp Ser Ser Met Ser  
 45 50 55

gaa gac gcg tcg gtg gcc gac atg gag agg gcg cag ctg gag gag gag 244  
 Glu Asp Ala Ser Val Ala Asp Met Glu Arg Ala Gln Leu Glu Glu Glu  
 60 65 70

gcg gcg gct gcg gag gag agg ccg ctg gtg ttc ctg tgc tcc ggc tgc 292  
 Ala Ala Ala Ala Glu Glu Arg Pro Leu Val Phe Leu Cys Ser Gly Cys  
 75 80 85

cgg cgg ccg ctg ggc gac tcg ctg agc tgg gtg gcc agc cag gag gac 340  
 Arg Arg Pro Leu Gly Asp Ser Leu Ser Trp Val Ala Ser Gln Glu Asp  
 90 95 100

acc aac tgc atc ctg ctt cgc tgt gtt tcc tgt aat gtt tct gtg gat 388  
 Thr Asn Cys Ile Leu Leu Arg Cys Val Ser Cys Asn Val Ser Val Asp  
 105 110 115 120

aag gaa cag aag cta tcc aaa cgt gaa aag gaa aat ggt tgc gtc ctt 436  
 Lys Glu Gln Lys Leu Ser Lys Arg Glu Lys Glu Asn Gly Cys Val Leu  
 125 130 135

gag act ttg tgc tgc gcg ggg tgc tca ctc aat ctt ggc tac gtg tac 484  
 Glu Thr Leu Cys Cys Ala Gly Cys Ser Leu Asn Leu Gly Tyr Val Tyr  
 140 145 150

aga tgc acg ccc aag aat ctt gat tac aag aga gac ttg ttt tgc ctc 532  
 Arg Cys Thr Pro Lys Asn Leu Asp Tyr Lys Arg Asp Leu Phe Cys Leu  
 155 160 165

agt gtt gaa gcc att gaa agt tat gtt tta ggg tcc tct gaa aag caa 580  
 Ser Val Glu Ala Ile Glu Ser Tyr Val Leu Gly Ser Ser Glu Lys Gln  
 170 175 180

att gtg tca gaa gat aaa gag ctt ttt aat ctt gaa agc aga gtt gaa 628  
 Ile Val Ser Glu Asp Lys Glu Leu Phe Asn Leu Glu Ser Arg Val Glu  
 185 190 195 200

ata gaa aag tct cta aca cag atg gaa gat gtc ttg aaa gca tta caa 676  
 Ile Glu Lys Ser Leu Thr Gln Met Glu Asp Val Leu Lys Ala Leu Gln  
 205 210 215

atg aag ctg tgg gag gcc gaa tcc aaa ttg tcc ttt gcc act tgt aaa 724  
 Met Lys Leu Trp Glu Ala Glu Ser Lys Leu Ser Phe Ala Thr Cys Lys  
 220 225 230

agc tga actctagtct gtgtcctcca ttctgcccc gcccttcctc cccttatttg 780  
 Ser

ttaaatgaag caacatagtg agacgtcgtc tctacaaaaa aaaaaagaaa aaaaaaaatt 840

agccaggcat gcgaaacgct gaggtgggag gatcagatga gcttgggagg ttgaggctgc 900

agtgagcctt ggtcatgcca ctactgcgtt ctagtctggg caacagagtg agaccttctc 960

tcaaaaaaaaa aaccctaaat tgtagaatta cttctatagc tatattttat gataaagaag 1020

tgattgtttc tcaaaatcgc atttttaaaga cgttttatgg tacttgttgg aattgggact 1080

taggagtttt gattttgata agaaactggg atgattttct gaactttttt tcctctgtat 1140

cacatttatt tactattttt aaaaactttg acatttaaca cttgggacaa catttattat 1200

aaatgataag aaaaatctta gaggtttgtc taccacagtg gtcattggaat cttctctgaa 1260

aactaatcca taaagttccc tggagaaatt ggtcagaatg atctgtcaga accatttgaa 1320

aacttgctca agagcagttg cttatatata gtaggatttt actttttcct gcttatgtac 1380

tactatatgc ttaaaaaacc tggaggaata cttaccaaaag aggagtaacc atctctgagg 1440

gtgggattct gggggaattt ttgttttttt ctgttttcta taatgtgaaa cttttgtagt 1500

atgtattttt ctaattgaag agaataaaga ttaaaacaaa gtg 1543

<210> 82  
 <211> 233  
 <212> PRT  
 <213> Homo sapiens

<400> 82  
 Met Ala Gly Val Arg Ser Leu Arg Cys Ser Arg Gly Cys Ala Gly Gly

1	5	10	15
Cys Glu Cys Gly Asp Lys Gly Lys Cys Ser Asp Ser Ser Leu Leu Gly			
	20	25	30
Lys Arg Leu Ser Glu Asp Ser Ser Arg His Gln Leu Leu Gln Lys Trp			
	35	40	45
Ala Ser Met Trp Ser Ser Met Ser Glu Asp Ala Ser Val Ala Asp Met			
	50	55	60
Glu Arg Ala Gln Leu Glu Glu Glu Ala Ala Ala Glu Glu Arg Pro			
	65	70	75
Leu Val Phe Leu Cys Ser Gly Cys Arg Arg Pro Leu Gly Asp Ser Leu			
	85	90	95
Ser Trp Val Ala Ser Gln Glu Asp Thr Asn Cys Ile Leu Leu Arg Cys			
	100	105	110
Val Ser Cys Asn Val Ser Val Asp Lys Glu Gln Lys Leu Ser Lys Arg			
	115	120	125
Glu Lys Glu Asn Gly Cys Val Leu Glu Thr Leu Cys Cys Ala Gly Cys			
	130	135	140
Ser Leu Asn Leu Gly Tyr Val Tyr Arg Cys Thr Pro Lys Asn Leu Asp			
	145	150	155
Tyr Lys Arg Asp Leu Phe Cys Leu Ser Val Glu Ala Ile Glu Ser Tyr			
	165	170	175
Val Leu Gly Ser Ser Glu Lys Gln Ile Val Ser Glu Asp Lys Glu Leu			
	180	185	190
Phe Asn Leu Glu Ser Arg Val Glu Ile Glu Lys Ser Leu Thr Gln Met			
	195	200	205
Glu Asp Val Leu Lys Ala Leu Gln Met Lys Leu Trp Glu Ala Glu Ser			
	210	215	220
Lys Leu Ser Phe Ala Thr Cys Lys Ser			
225	230		

<210> 83  
 <211> 1436  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (31)..(582)

<400> 83  
 acgtgaccca agccccagct tcgcgcaggg atg gag ccg gaa gag ggg acg ccc 54  
 Met Glu Pro Glu Glu Gly Thr Pro  
 1 5

ttg tgg cgg ctg cag aag ctg ccg gcc gag ctg ggc ccg cag ctt ctt 102  
 Leu Trp Arg Leu Gln Lys Leu Pro Ala Glu Leu Gly Pro Gln Leu Leu  
 10 15 20

cac aaa ata att gat ggc att tgt ggt cga gct tat cct gtg tac caa 150  
 His Lys Ile Ile Asp Gly Ile Cys Gly Arg Ala Tyr Pro Val Tyr Gln  
 25 30 35 40

gat tat cac act gtt tgg gaa tca gaa gaa tgg atg cac gtt tta gaa 198  
 Asp Tyr His Thr Val Trp Glu Ser Glu Glu Trp Met His Val Leu Glu  
 45 50 55

gat att gcc aaa ttt ttc aaa gcc ata gtt ggt aaa aac tta cct gat	246
Asp Ile Ala Lys Phe Phe Lys Ala Ile Val Gly Lys Asn Leu Pro Asp	
60 65 70	
gaa gag ata ttt cag cag ttg aat cag ttg aat tca ctt cat caa gaa	294
Glu Glu Ile Phe Gln Gln Leu Asn Gln Leu Asn Ser Leu His Gln Glu	
75 80 85	
act atc atg aaa tgc gtg aaa agt agg aaa gat gaa atc aaa cag gct	342
Thr Ile Met Lys Cys Val Lys Ser Arg Lys Asp Glu Ile Lys Gln Ala	
90 95 100	
ctg tca aga gaa ata gtt gct att tcc tct gca cag cta cag gat ttt	390
Leu Ser Arg Glu Ile Val Ala Ile Ser Ser Ala Gln Leu Gln Asp Phe	
105 110 115 120	
gat tgg cag gta aag ctt gca ctt tcc agt gac aag att gct gca tta	438
Asp Trp Gln Val Lys Leu Ala Leu Ser Ser Asp Lys Ile Ala Ala Leu	
125 130 135	
cga atg cca ctt tta agc ctg cat cta gat gta aaa gaa aat ggt gaa	486
Arg Met Pro Leu Leu Ser Leu His Leu Asp Val Lys Glu Asn Gly Glu	
140 145 150	
gta aaa cct tat tct att gaa atg agt aga gag gag ctg cag aat cta	534
Val Lys Pro Tyr Ser Ile Glu Met Ser Arg Glu Glu Leu Gln Asn Leu	
155 160 165	
ata cag tcc ttg gaa gca gcg aat aag gtg gtc ctg cag ttg aaa taa	582
Ile Gln Ser Leu Glu Ala Ala Asn Lys Val Val Leu Gln Leu Lys	
170 175 180	
ctggaaatga tgaataccag tcctatcaga ttttattgct ccaacttata tggcagagtg	642
aatactgcgt gttcagaaac cttgtgatgt cttgactgtt gcaccaggct gagaaagcag	702
caatattgat attataaaga taaaaattta tcaacattcc ttaacaggaa attacatggt	762
tgagaggaaa tgcataaaat gaaagatgaa aaatctatag tagcagttta tattttcatg	822
attgttttgc ctcatattatt aaatatttga gaaatctttg gagatacata gttttattga	882
aagctaaaaa taggttctaa agtaatgtaa aaatataaag cacaaatata cttgaatatt	942
gcttaaagaa ttgtgtgaat agcaacatat attatggata tatactttgt gatattttta	1002
aaaaataatt ttttcaaaga atgtataagc tgcataatata actcaggaga ttccatgtct	1062
ttctcatatt tcagaggaaa gattataaaa tataaaattt cttagagaac acctctttgt	1122
cagagataaa caagaacaaa tactctaaac ttatgtgaac agttttgagt ttatgaattc	1182
tagaaactaa aatcaagaat acagaaaaat gaaaataaca ttttacttct gcgcttctat	1242
gtttgggaaa cattgctctg ataaaaaata gctgtcatta tgcagtgtgt atattcaa	1302
atgagataag actatgtaca catccacttt tgtaataaaa ctcaatattg aatacttttg	1362

gatgttaaatt tcattggaaa aacaaacccat ttgtaacctc agttaacttt aacaacaagc 1422

attctgagca aatg 1436

<210> 84  
<211> 183  
<212> PRT  
<213> Homo sapiens

<400> 84  
Met Glu Pro Glu Glu Gly Thr Pro Leu Trp Arg Leu Gln Lys Leu Pro  
1 5 10 15  
Ala Glu Leu Gly Pro Gln Leu Leu His Lys Ile Ile Asp Gly Ile Cys  
20 25 30  
Gly Arg Ala Tyr Pro Val Tyr Gln Asp Tyr His Thr Val Trp Glu Ser  
35 40 45  
Glu Glu Trp Met His Val Leu Glu Asp Ile Ala Lys Phe Phe Lys Ala  
50 55 60  
Ile Val Gly Lys Asn Leu Pro Asp Glu Glu Ile Phe Gln Gln Leu Asn  
65 70 75 80  
Gln Leu Asn Ser Leu His Gln Glu Thr Ile Met Lys Cys Val Lys Ser  
85 90 95  
Arg Lys Asp Glu Ile Lys Gln Ala Leu Ser Arg Glu Ile Val Ala Ile  
100 105 110  
Ser Ser Ala Gln Leu Gln Asp Phe Asp Trp Gln Val Lys Leu Ala Leu  
115 120 125  
Ser Ser Asp Lys Ile Ala Ala Leu Arg Met Pro Leu Leu Ser Leu His  
130 135 140  
Leu Asp Val Lys Glu Asn Gly Glu Val Lys Pro Tyr Ser Ile Glu Met  
145 150 155 160  
Ser Arg Glu Glu Leu Gln Asn Leu Ile Gln Ser Leu Glu Ala Ala Asn  
165 170 175  
Lys Val Val Leu Gln Leu Lys  
180

<210> 85  
<211> 1357  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (102)..(1244)

<400> 85  
ggtttccggc gagagggcca gagtgagtgt ttacaccggc ggcagtgcgg ccgggttcct 60  
tccgcgggac ggggagaaag agagagcgcg aaagagagag g atg tct ctc tca gac 116  
Met Ser Leu Ser Asp  
1 5

tgg cac ctg gcg gtg aag ctg gct gac cag cca ctt act cca aag tct 164  
Trp His Leu Ala Val Lys Leu Ala Asp Gln Pro Leu Thr Pro Lys Ser  
10 15 20

att ctt cgg ttg cca gag aca gaa ctg gga gaa tac tcg cta ggg ggc	212
Ile Leu Arg Leu Pro Glu Thr Glu Leu Gly Glu Tyr Ser Leu Gly Gly	
25 30 35	
tat agt att tca ttt ctg aag cag ctt att gct ggc aaa ctc cag gag	260
Tyr Ser Ile Ser Phe Leu Lys Gln Leu Ile Ala Gly Lys Leu Gln Glu	
40 45 50	
tct gtt cca gac cct gag ctg att gat ctg atc tac tgt ggt cgg aag	308
Ser Val Pro Asp Pro Glu Leu Ile Asp Leu Ile Tyr Cys Gly Arg Lys	
55 60 65	
cta aaa gat gac cag aca ctt gac ttc tat ggc att caa cct ggg tcc	356
Leu Lys Asp Asp Gln Thr Leu Asp Phe Tyr Gly Ile Gln Pro Gly Ser	
70 75 80 85	
act gtc cat gtt ctg cga aag tcc tgg cct gaa cct gat cag aaa ccg	404
Thr Val His Val Leu Arg Lys Ser Trp Pro Glu Pro Asp Gln Lys Pro	
90 95 100	
gaa cct gtg gac aaa gtg gct gcc atg aga gag ttc cgg gtg ttg cac	452
Glu Pro Val Asp Lys Val Ala Ala Met Arg Glu Phe Arg Val Leu His	
105 110 115	
act gcc ctg cac agc agc tcc tct tac agg gag gcg gtc ttt aag atg	500
Thr Ala Leu His Ser Ser Ser Ser Tyr Arg Glu Ala Val Phe Lys Met	
120 125 130	
ctc agc aat aag gag tct ctg gat cag atc att gtg gcc acc cca ggc	548
Leu Ser Asn Lys Glu Ser Leu Asp Gln Ile Ile Val Ala Thr Pro Gly	
135 140 145	
ctc agc agt gac cct att gct ctt ggg gtt ctc cag gac aag gac ctc	596
Leu Ser Ser Asp Pro Ile Ala Leu Gly Val Leu Gln Asp Lys Asp Leu	
150 155 160 165	
ttc tct gtc ttc gct gat ccc aat atg ctt gat acg ttg gtg cct gct	644
Phe Ser Val Phe Ala Asp Pro Asn Met Leu Asp Thr Leu Val Pro Ala	
170 175 180	
cac cca gcc ctc gtc aat gcc att gtc ctg gtt ctg cac tcc gta gca	692
His Pro Ala Leu Val Asn Ala Ile Val Leu Val Leu His Ser Val Ala	
185 190 195	
ggc agt gcc cca atg cct ggg act gac tcc tct tcc cgg agc atg ccc	740
Gly Ser Ala Pro Met Pro Gly Thr Asp Ser Ser Ser Arg Ser Met Pro	
200 205 210	
tcc agc tca tac cgg gat atg cca ggt ggc ttc ctg ttt gaa ggg ctc	788
Ser Ser Ser Tyr Arg Asp Met Pro Gly Gly Phe Leu Phe Glu Gly Leu	
215 220 225	
tca gat gat gag gat gac ttt cac cca aac acc agg tcc aca ccc tct	836
Ser Asp Asp Glu Asp Asp Phe His Pro Asn Thr Arg Ser Thr Pro Ser	
230 235 240 245	

agc agt act ccc agc tcc cgc cca gcc tcc ctg ggg tac agt gga gct 884  
 Ser Ser Thr Pro Ser Ser Arg Pro Ala Ser Leu Gly Tyr Ser Gly Ala  
 250 255 260

gct ggg ccc cgg ccc atc acc cag agt gag ctg gcc acc gcc ttg gcc 932  
 Ala Gly Pro Arg Pro Ile Thr Gln Ser Glu Leu Ala Thr Ala Leu Ala  
 265 270 275

ctg gcc agc act ccg gag agc agc tct cac aca ccg act cct ggc acc 980  
 Leu Ala Ser Thr Pro Glu Ser Ser Ser His Thr Pro Thr Pro Gly Thr  
 280 285 290

cag ggt cat tcc tca ggg acc tca cca atg tcc tct ggt gtc cag tca 1028  
 Gln Gly His Ser Ser Gly Thr Ser Pro Met Ser Ser Gly Val Gln Ser  
 295 300 305

ggg acg ccc atc acc aat gat ctc ttc agc caa gcc cta cag cat gcc 1076  
 Gly Thr Pro Ile Thr Asn Asp Leu Phe Ser Gln Ala Leu Gln His Ala  
 310 315 320 325

ctt cag gcc tct ggg cag ccc agc ctt cag agc cag tgg cag ccc cag 1124  
 Leu Gln Ala Ser Gly Gln Pro Ser Leu Gln Ser Gln Trp Gln Pro Gln  
 330 335 340

ctg cag cag cta cgt gac atg ggc atc cag gac gat gag ctg agc ctg 1172  
 Leu Gln Gln Leu Arg Asp Met Gly Ile Gln Asp Asp Glu Leu Ser Leu  
 345 350 355

cgg gcc ctg cag gcc acc ggt ggg gac atc caa gca gcc ctg gag ctc 1220  
 Arg Ala Leu Gln Ala Thr Gly Gly Asp Ile Gln Ala Ala Leu Glu Leu  
 360 365 370

atc ttt gct gga gga gcc cca tga actccctgct tcccctgaac ccccagcaag 1274  
 Ile Phe Ala Gly Gly Ala Pro  
 375 380

ttgcagaggc tactgccctt gggaggcact catgaaggtg cctccatctc tcccttcccc 1334

aatatacctg atggtcaact ctc 1357

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 <212> PRT  
 <213> Homo sapiens

<400> 86  
 Met Ser Leu Ser Asp Trp His Leu Ala Val Lys Leu Ala Asp Gln Pro  
 1 5 10 15  
 Leu Thr Pro Lys Ser Ile Leu Arg Leu Pro Glu Thr Glu Leu Gly Glu  
 20 25 30  
 Tyr Ser Leu Gly Gly Tyr Ser Ile Ser Phe Leu Lys Gln Leu Ile Ala  
 35 40 45  
 Gly Lys Leu Gln Glu Ser Val Pro Asp Pro Glu Leu Ile Asp Leu Ile  
 50 55 60  
 Tyr Cys Gly Arg Lys Leu Lys Asp Asp Gln Thr Leu Asp Phe Tyr Gly  
 65 70 75 80



cgg cct aat tcc agg gcg gat ggt ggt gat gga agc agg tgg aat tat	157
Arg Pro Asn Ser Arg Ala Asp Gly Gly Asp Gly Ser Arg Trp Asn Tyr	
15 20 25	
gcc ctg ttg gtt cca atg ctg gga ttg gct gct ttt cgt tgg att tgg	205
Ala Leu Leu Val Pro Met Leu Gly Leu Ala Ala Phe Arg Trp Ile Trp	
30 35 40	
tct agg gag tcc cag aaa gaa gta gaa aaa gag aga gaa gcc tac cgt	253
Ser Arg Glu Ser Gln Lys Glu Val Glu Lys Glu Arg Glu Ala Tyr Arg	
45 50 55 60	
cgg aga act gct gct ttt caa cag gat ctg gaa gcc aag tac cac gcc	301
Arg Arg Thr Ala Ala Phe Gln Gln Asp Leu Glu Ala Lys Tyr His Ala	
65 70 75	
atg atc tca gaa aat cgg cgt gct gtc gct cag ttg tcc ttg gaa ctc	349
Met Ile Ser Glu Asn Arg Arg Ala Val Ala Gln Leu Ser Leu Glu Leu	
80 85 90	
gaa aag gaa caa aac aga act gct agt tac cga gaa gcc ctt atc tct	397
Glu Lys Glu Gln Asn Arg Thr Ala Ser Tyr Arg Glu Ala Leu Ile Ser	
95 100 105	
cag gga cgc aag ttg gta gaa gaa aag aag ctt ctg gaa cag gaa cgg	445
Gln Gly Arg Lys Leu Val Glu Glu Lys Lys Leu Leu Glu Gln Glu Arg	
110 115 120	
gcc cag gtg atg caa gaa aaa aga cag gtg cag cct ttg aga agt gcg	493
Ala Gln Val Met Gln Glu Lys Arg Gln Val Gln Pro Leu Arg Ser Ala	
125 130 135 140	
tat ttg agc tgc ctg caa agg gaa gaa aac tgg caa agg aga gcc agg	541
Tyr Leu Ser Cys Leu Gln Arg Glu Glu Asn Trp Gln Arg Arg Ala Arg	
145 150 155	
ctt ttg ctg aaa gaa ttt gaa gct gtt ctc aca gaa aga cag aat atc	589
Leu Leu Leu Lys Glu Phe Glu Ala Val Leu Thr Glu Arg Gln Asn Ile	
160 165 170	
tac tgc agt ctg ttt ctt cct cgc agc aag cgg ctg gag ata gag aag	637
Tyr Cys Ser Leu Phe Leu Pro Arg Ser Lys Arg Leu Glu Ile Glu Lys	
175 180 185	
agc tta ctg gtg cga gcg tcc gtc gac ccc gtc gcc gct gac cta gag	685
Ser Leu Leu Val Arg Ala Ser Val Asp Pro Val Ala Ala Asp Leu Glu	
190 195 200	
atg gca gcc ggt ctc acc gac ata ttt cag cat gat aca tac tgt ggt	733
Met Ala Ala Gly Leu Thr Asp Ile Phe Gln His Asp Thr Tyr Cys Gly	
205 210 215 220	
gat gtc tgg aac acc aac aaa cgc cag aat ggc aga ctc atg tgg ctc	781
Asp Val Trp Asn Thr Asn Lys Arg Gln Asn Gly Arg Leu Met Trp Leu	
225 230 235	
tat ctc aaa tac tgg gaa ctc gtt gtc gaa ctg aag aag ttt aag aga	829

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Tyr Leu Lys Tyr Trp Glu Leu Val Val Glu Leu Lys Lys Phe Lys Arg  
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gta gag gaa gcc ata cta gaa aag taa gacaagagtg aaatcaaact 876  
Val Glu Glu Ala Ile Leu Glu Lys  
255 260

gcttttagtg actcgaggcc aggcagtcac gcgccttctg ggtctccggc gtcttccggt 936  
cccgtgctgc ccgtgtcatg gccacaccgt cacccttcag cagcgacctc cactcccgcc 996  
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<212> PRT  
<213> Homo sapiens

<400> 88  
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35 40 45  
Gln Lys Glu Val Glu Lys Glu Arg Glu Ala Tyr Arg Arg Arg Thr Ala  
50 55 60  
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65 70 75 80  
Asn Arg Arg Ala Val Ala Gln Leu Ser Leu Glu Leu Glu Lys Glu Gln  
85 90 95  
Asn Arg Thr Ala Ser Tyr Arg Glu Ala Leu Ile Ser Gln Gly Arg Lys  
100 105 110  
Leu Val Glu Glu Lys Lys Leu Leu Glu Gln Glu Arg Ala Gln Val Met  
115 120 125  
Gln Glu Lys Arg Gln Val Gln Pro Leu Arg Ser Ala Tyr Leu Ser Cys  
130 135 140  
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145 150 155 160  
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Phe Leu Pro Arg Ser Lys Arg Leu Glu Ile Glu Lys Ser Leu Leu Val  
180 185 190  
Arg Ala Ser Val Asp Pro Val Ala Ala Asp Leu Glu Met Ala Ala Gly

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Leu Thr Asp Ile Phe Gln His Asp Thr Tyr Cys Gly Asp Val Trp Asn						
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Thr Asn Lys Arg Gln Asn Gly Arg Leu Met Trp Leu Tyr Leu Lys Tyr						
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Ile Leu Glu Lys						
260						

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 <212> DNA  
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 <222> (152)..(976)

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 agctgctgct gctccctgcc cagccccagc c atg aaa ctg ccc aag ggg acc 172  
 Met Lys Leu Pro Lys Gly Thr  
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 agg agc tct gtg tac ttt gca cag cac cca gaa aag gag cca ttg ccc 220  
 Arg Ser Ser Val Tyr Phe Ala Gln His Pro Glu Lys Glu Pro Leu Pro  
 10 15 20  
 tca agg cag gag gtc aag cag acc cct gtc atc atg gcc aag atc aaa 268  
 Ser Arg Gln Glu Val Lys Gln Thr Pro Val Ile Met Ala Lys Ile Lys  
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 ggt ccg ggg ccc gcc aag tac ctc cgg cca tcc tgc acg ggc tac ata 316  
 Gly Pro Gly Pro Ala Lys Tyr Leu Arg Pro Ser Cys Thr Gly Tyr Ile  
 40 45 50 55  
 gat cat gac atc tcc atg ttc aag gca cca gct tat acc ctg cat agc 364  
 Asp His Asp Ile Ser Met Phe Lys Ala Pro Ala Tyr Thr Leu His Ser  
 60 65 70  
 cgg cac tca gag aag cgg atg gtg tgc cac agc agc cct ggg cct tgc 412  
 Arg His Ser Glu Lys Arg Met Val Cys His Ser Ser Pro Gly Pro Cys  
 75 80 85  
 tat ctc ttg gat ccc aaa ata act cgg ttt gga atg tcc agc tgc ccg 460  
 Tyr Leu Leu Asp Pro Lys Ile Thr Arg Phe Gly Met Ser Ser Cys Pro  
 90 95 100  
 cag gtc ccc atg gag gag cgc atc tcc aac ctg cgc ctg aac ccc acc 508  
 Gln Val Pro Met Glu Glu Arg Ile Ser Asn Leu Arg Leu Asn Pro Thr  
 105 110 115

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Pro Glu Lys Glu Pro Leu Pro Ser Arg Gln Glu Val Lys Gln Thr Pro



Lys Glu Leu Leu Arg Ala Lys Leu Ile Glu Cys Gly Trp Lys Asp Gln  
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 Leu Lys Ala His Cys Lys Glu Val Ile Lys Glu Lys Gly Leu Glu His  
 50 55 60

gtt act gtt gat gac ttg gtg gct gaa atc act cca aaa ggc aga gcc 363  
 Val Thr Val Asp Asp Leu Val Ala Glu Ile Thr Pro Lys Gly Arg Ala  
 65 70 75

ctg gta cct gac agt gta aag aag gag ctc cta caa aga ata aga aca 411  
 Leu Val Pro Asp Ser Val Lys Lys Glu Leu Leu Gln Arg Ile Arg Thr  
 80 85 90

ttc ctt gct cag cat gcc agc ctt taa gattgaatta gattgtgttg 458  
 Phe Leu Ala Gln His Ala Ser Leu  
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aaatcctttt ttgtatgatg gt 540

<210> 92  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

<400> 92  
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 Leu Arg Ala Lys Leu Ile Glu Cys Gly Trp Lys Asp Gln Leu Lys Ala  
 35 40 45  
 His Cys Lys Glu Val Ile Lys Glu Lys Gly Leu Glu His Val Thr Val  
 50 55 60  
 Asp Asp Leu Val Ala Glu Ile Thr Pro Lys Gly Arg Ala Leu Val Pro  
 65 70 75 80  
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<210> 93  
 <211> 1059  
 <212> DNA  
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<220>  
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 <222> (33)..(869)

<400> 93  
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Glu Thr Gln Val Ala Ala Trp Leu Lys Lys Ile Phe Gly Asp His Pro  
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att cca cag tat gag gtg aac cca cgg acc aca gag att tta cat cac 149  
Ile Pro Gln Tyr Glu Val Asn Pro Arg Thr Thr Glu Ile Leu His His  
25 30 35

ctt tca gaa cgc aac agg gtc cgg gac agg gat gtc tac ctg gta ata 197  
Leu Ser Glu Arg Asn Arg Val Arg Asp Arg Asp Val Tyr Leu Val Ile  
40 45 50 55

gag gac ttg aag cag aaa gca agt gaa tac gag tca gaa gcc aag tat 245  
Glu Asp Leu Lys Gln Lys Ala Ser Glu Tyr Glu Ser Glu Ala Lys Tyr  
60 65 70

ctt caa gac ctt ctc atg gag agt gtg aat ttt tcc ccc gcc aat ctc 293  
Leu Gln Asp Leu Leu Met Glu Ser Val Asn Phe Ser Pro Ala Asn Leu  
75 80 85

tct agc act ggt tcc agg tat ctg aat gct ttg gtt gac agt gcg gtg 341  
Ser Ser Thr Gly Ser Arg Tyr Leu Asn Ala Leu Val Asp Ser Ala Val  
90 95 100

gcc ctt gaa aca aag gat acc tcg cta gct agt ttt atc cct gca gtg 389  
Ala Leu Glu Thr Lys Asp Thr Ser Leu Ala Ser Phe Ile Pro Ala Val  
105 110 115

aat gat ttg acc tct gat ctc ttt cgt acc aaa tcc aaa agt gaa gaa 437  
Asn Asp Leu Thr Ser Asp Leu Phe Arg Thr Lys Ser Lys Ser Glu Glu  
120 125 130 135

atc aag att gaa ctg gaa aaa ctt gaa aaa aat tta act gca act tta 485  
Ile Lys Ile Glu Leu Glu Lys Leu Glu Lys Asn Leu Thr Ala Thr Leu  
140 145 150

gta tta gaa aaa tgt cta caa gag gat gtc aag aaa gca gag ttg cat 533  
Val Leu Glu Lys Cys Leu Gln Glu Asp Val Lys Lys Ala Glu Leu His  
155 160 165

ctg tct aca gaa agg gcc aaa gtt gat aat cgt cgt cag aac atg gac 581  
Leu Ser Thr Glu Arg Ala Lys Val Asp Asn Arg Arg Gln Asn Met Asp  
170 175 180

ttt cta aaa gca aag tca gag gaa ttc aga ttt gga atc aag gct gca 629  
Phe Leu Lys Ala Lys Ser Glu Glu Phe Arg Phe Gly Ile Lys Ala Ala  
185 190 195

gag gag caa ctt tca gcc aga ggc atg gat gct tct ctg tct cat cag 677  
Glu Glu Gln Leu Ser Ala Arg Gly Met Asp Ala Ser Leu Ser His Gln  
200 205 210 215

tcc tta gta gca cta tca gag aaa ctg gca aga tta aag caa cag act 725  
Ser Leu Val Ala Leu Ser Glu Lys Leu Ala Arg Leu Lys Gln Gln Thr



Ala Arg Leu Lys Gln Gln Thr Ile Pro Leu Lys Lys Lys Leu Glu Ser  
 225 230 235 240  
 Tyr Leu Asp Leu Met Pro Asn Pro Ser Leu Ala Gln Val Lys Ile Glu  
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 Glu Ala Lys Arg Glu Leu Asp Ser Ile Glu Ala Glu Leu Thr Arg Arg  
 260 265 270  
 Val Asp Met Met Glu Leu  
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<210> 95  
 <211> 782  
 <212> DNA  
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<220>  
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 <222> (103)..(384)

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 Met Ser Gly Leu  
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 cgc gtc tac agc acg tcg gtc acc ggc tcc cgc gaa atc aag tcc cag 162  
 Arg Val Tyr Ser Thr Ser Val Thr Gly Ser Arg Glu Ile Lys Ser Gln  
 5 10 15 20  
 cag agc gag gtg acc cga atc ctg gat ggg aag cgc atc caa tac cag 210  
 Gln Ser Glu Val Thr Arg Ile Leu Asp Gly Lys Arg Ile Gln Tyr Gln  
 25 30 35  
 cta gtg gac atc tcc cag gac aac gcc ctg agg gat gag atg cga gcc 258  
 Leu Val Asp Ile Ser Gln Asp Asn Ala Leu Arg Asp Glu Met Arg Ala  
 40 45 50  
 ttg gca ggc aac ccc aag gcc acc cca ccc cag att gtc aac ggg gac 306  
 Leu Ala Gly Asn Pro Lys Ala Thr Pro Pro Gln Ile Val Asn Gly Asp  
 55 60 65  
 cag tac tgt ggg gac tat gag ctg ttc gtg gag gct gtg gaa caa aac 354  
 Gln Tyr Cys Gly Asp Tyr Glu Leu Phe Val Glu Ala Val Glu Gln Asn  
 70 75 80  
 acg ctg cag gag ttc ctg aag ctg gct tga gtcaagcctg tccagagttc 404  
 Thr Leu Gln Glu Phe Leu Lys Leu Ala  
 85 90  
 ccctgctgga ctccatcacc aactcccc cagccttcac ctggccatga aggacctttt 464  
 gaccaactcc ctgtcattcc taacctaac ttagagtccc tcccccaatg caggccactt 524  
 ctctccctc ctctctaaat gtagtcccct ctctccatc taaaggcaac attccttacc 584

cattagtctc agaaaattgtc ttaagcaaca gcccctaatg ctggtgccc ccagccaagc 644  
 attggggccc ccatcctgcc tggcactggc tgatgggcac ctctgttggt tccatcagcc 704  
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 atgtcctgtt ccattggc 782

<210> 96  
 <211> 93  
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 <213> Homo sapiens

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 20 25 30  
 Ile Gln Tyr Gln Leu Val Asp Ile Ser Gln Asp Asn Ala Leu Arg Asp  
 35 40 45  
 Glu Met Arg Ala Leu Ala Gly Asn Pro Lys Ala Thr Pro Pro Gln Ile  
 50 55 60  
 Val Asn Gly Asp Gln Tyr Cys Gly Asp Tyr Glu Leu Phe Val Glu Ala  
 65 70 75 80  
 Val Glu Gln Asn Thr Leu Gln Glu Phe Leu Lys Leu Ala  
 85 90

<210> 97  
 <211> 417  
 <212> DNA  
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 Glu Gly Ala Gly Pro Tyr Val Asp Leu Asp Glu Ala Gly Gly Ser Thr 25  
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 ggg ctc ttg atg gac ttg gca gcc aat gaa aag gcc gtt cat gca gac 147  
 Gly Leu Leu Met Asp Leu Ala Ala Asn Glu Lys Ala Val His Ala Asp 40  
 30 35  
 ttt ttt aac gat ttt gaa gat ctt ttt gat gat gat gac atc cag tga 195  
 Phe Phe Asn Asp Phe Glu Asp Leu Phe Asp Asp Asp Asp Ile Gln 55  
 45 50  
 gatgccctct ggctgcaggc ggggcccaagc ccttggtaca gagccgcagt gtgagcctgc 255

gcaggacagt ttcaggtggt tttaaagaac acgtggaaat cccttgaatt taggacctgg 315  
 ttaaccagaa agataagact gttcttaacg acctagatga ttctgttcat ctctgaacgg 375  
 gatcaggttt tgtcctcact ccaattaaaa gaaagcaatg tc 417

<210> 98  
 <211> 57  
 <212> PRT  
 <213> Homo sapiens

<400> 98  
 Met Lys Pro Ala Val Asp Glu Met Phe Pro Glu Gly Ala Gly Pro Tyr  
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 Val Asp Leu Asp Glu Ala Gly Gly Ser Thr Gly Leu Leu Met Asp Leu  
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 Ala Ala Asn Glu Lys Ala Val His Ala Asp Phe Phe Asn Asp Phe Glu  
 35 40 45  
 Asp Leu Phe Asp Asp Asp Asp Ile Gln  
 50 55

<210> 99  
 <211> 697  
 <212> DNA  
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 <222> (65)..(412)

<400> 99  
 aagacatttc ctgctcgaa ccttggttac taatttccac tgcttttaag gccctgcact 60  
 gaaa atg caa gct cag gcg ccg gtg gtc gtt gtg acc caa cct gga gtc 109  
 Met Gln Ala Gln Ala Pro Val Val Val Val Thr Gln Pro Gly Val  
 1 5 10 15  
 ggt ccc ggt ccg gcc ccc cag aac tcc aac tgg cag aca ggc atg tgt 157  
 Gly Pro Gly Pro Ala Pro Gln Asn Ser Asn Trp Gln Thr Gly Met Cys  
 20 25 30  
 gac tgt ttc agc gac tgc gga gtc tgt ctc tgt ggc aca ttt tgt ttc 205  
 Asp Cys Phe Ser Asp Cys Gly Val Cys Leu Cys Gly Thr Phe Cys Phe  
 35 40 45  
 ccg tgc ctt ggg tgt caa gtt gca gct gat atg aat gaa tgc tgt ctg 253  
 Pro Cys Leu Gly Cys Gln Val Ala Ala Asp Met Asn Glu Cys Cys Leu  
 50 55 60  
 tgt gga aca agc gtc gca atg agg act ctc tac agg acc cga tat ggc 301  
 Cys Gly Thr Ser Val Ala Met Arg Thr Leu Tyr Arg Thr Arg Tyr Gly  
 65 70 75  
 atc cct gga tct att tgt gat gac tat atg gca act ctt tgc tgt cct 349  
 Ile Pro Gly Ser Ile Cys Asp Asp Tyr Met Ala Thr Leu Cys Cys Pro

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80 85 90 95  
cat tgt act ctt tgc caa atc aag aga gat atc aac aga agg aga gcc 397  
His Cys Thr Leu Cys Gln Ile Lys Arg Asp Ile Asn Arg Arg Arg Ala  
100 105 110  
atg cgt act ttc taa aaactgatgg tgaaaagctc ttaccgaagc aacaaaattc 452  
Met Arg Thr Phe  
115  
agcagacacc tcttcagctt gagttcttca ccatcttttg caactgaaat atgatggata 512  
tgcttaagta caactgatgg catgaaaaaa atcaaatttt tgatttatta taaatgaatg 572  
ttgtccctga acttagctaa atggtgcaac ttagtttctc cttgctttca tattatcgaa 632  
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ctgat 697

<210> 100  
<211> 115  
<212> PRT  
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Cys Phe Ser Asp Cys Gly Val Cys Leu Cys Gly Thr Phe Cys Phe Pro  
35 40 45  
Cys Leu Gly Cys Gln Val Ala Ala Asp Met Asn Glu Cys Cys Leu Cys  
50 55 60  
Gly Thr Ser Val Ala Met Arg Thr Leu Tyr Arg Thr Arg Tyr Gly Ile  
65 70 75 80  
Pro Gly Ser Ile Cys Asp Asp Tyr Met Ala Thr Leu Cys Cys Pro His  
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Cys Thr Leu Cys Gln Ile Lys Arg Asp Ile Asn Arg Arg Arg Ala Met  
100 105 110  
Arg Thr Phe  
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<210> 101  
<211> 1504  
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<221> CDS  
<222> (462)..(794)

<400> 101  
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 35 40 45  
 Gly Ser Glu Arg Phe Leu Cys Glu Ser Val Phe Ser Tyr Gln Val Ala  
 50 55 60  
 Ser Thr Leu Lys Gln Val Lys His Asp Gln Gln Val Ala Arg Met Glu  
 65 70 75 80  
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 Lys Pro Ile Glu Gln Leu Leu Gly Phe Thr Pro Ser Ser Gly  
 100 105 110

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 ggg atg tgg tgt ggc tgt gat ggg aac ctg agt gtc cag acc tat tta 168  
 Met Trp Cys Gly Cys Asp Gly Asn Leu Ser Val Gln Thr Tyr Leu  
 1 5 10 15  
 ccg att gct cgt ggt ggg atc cct gcc ttc ctc ctc tgc ttg acc ccg 216  
 Pro Ile Ala Arg Gly Gly Ile Pro Ala Phe Leu Leu Cys Leu Thr Pro  
 20 25 30

ggt gtc cac gaa tgg tgt cct gac cct ctt ggg acg ctg aat gcc tgg 264  
 Gly Val His Glu Trp Cys Pro Asp Pro Leu Gly Thr Leu Asn Ala Trp  
                   35                                  40                                  45

agc tgt ctc gtg cct gct cgt ggt gcg atc ctt gtc ttc ctc cag tgc 312  
 Ser Cys Leu Val Pro Ala Arg Gly Ala Ile Leu Val Phe Leu Gln Cys  
                   50                                  55                                  60

tgg tcc cgg tcc gtc cat ggg cag agt cag gct gtt cat gag tgc tca 360  
 Trp Ser Arg Ser Val His Gly Gln Ser Gln Ala Val His Glu Cys Ser  
                   65                                  70                                  75

cct ggt aga ggg aag acc ctg aac gtc cag acc gtt ccc ctg acc ggc 408  
 Pro Gly Arg Gly Lys Thr Leu Asn Val Gln Thr Val Pro Leu Thr Gly  
                   80                                  85                                  90                                  95

cac gtg tgg act ctt ggt ggc tct gct gtc tca gcc cag cct ttc cgt 456  
 His Val Trp Thr Leu Gly Gly Ser Ala Val Ser Ala Gln Pro Phe Arg  
                                   100                                  105                                  110

ggc ctg aca ctg att gtg tgt ctg agt ttt ctg aat gtc cct cac tgt 504  
 Gly Leu Thr Leu Ile Val Cys Leu Ser Phe Leu Asn Val Pro His Cys  
                   115                                  120                                  125

cac tgg cct gac tac cgc tag acccccggtg tccacgatcg ctgactgcag 555  
 His Trp Pro Asp Tyr Arg  
                   130

atgaagcttg cccgcgcccc gtggctgagt gtctggagct gtctgctgac tgctggtggc 615  
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 cacgagagga agtctctgcg tgacgagtgc ctgattgtct ggagctgtct gcagagtgcc 735  
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 cccacgcaga tccatgatgg tttctggaag ccgaccaga gtgcctctca gagtcttctg 855  
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 Ala Val Arg Thr Leu Gln Ala Gly Gln Val Pro Gly Arg Pro Gly Leu  
                   20                  25                  30  
 Ala Tyr Ala Pro Leu Cys Pro Leu Ala Phe Lys Gly Phe Phe Pro Asn  
                   35                  40                  45  
 Leu Arg Pro Ser Ala Thr Cys Arg Phe Arg Arg Glu Pro Ala Ala Ser  
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 Phe Glu Pro Lys  
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 cgc tgc ctc ctg gct cca gtc gcc ccc aag ctg gtc cct ccg gtt cgg 99  
 Arg Cys Leu Leu Ala Pro Val Ala Pro Lys Leu Val Pro Pro Val Arg  
   15                  20                  25  
  
 gga gtg aag aag gga ttc cgc gcc gcc ttc cgc ttc cag aag gag tta 147  
 Gly Val Lys Lys Gly Phe Arg Ala Ala Phe Arg Phe Gln Lys Glu Leu  
   30                  35                  40                  45  
  
 gag cgg cag cgc ctt ctg cgg tgc ccg ccg ccg ccc gtg cgc cgt tca 195  
 Glu Arg Gln Arg Leu Leu Arg Cys Pro Pro Pro Pro Val Arg Arg Ser  
                   50                  55                  60  
  
 gag aag ccg aac tgg gat tac cat gca gaa ata caa gct ttt gga cat 243  
 Glu Lys Pro Asn Trp Asp Tyr His Ala Glu Ile Gln Ala Phe Gly His  
                   65                  70                  75  
  
 cgg tta cag gaa aac ttt tcc tta gat ctt ctc aaa act gca ttt gtt 291  
 Arg Leu Gln Glu Asn Phe Ser Leu Asp Leu Leu Lys Thr Ala Phe Val

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aat agc tgc tat att aaa agt gag gag gcc aaa cgc caa caa ctt ggg Asn Ser Cys Tyr Ile Lys Ser Glu Glu Ala Lys Arg Gln Gln Leu Gly 95 100 105			339
ata gag aaa gaa gct gtt ctt ctg aat ctt aaa agt aat caa gaa cta Ile Glu Lys Glu Ala Val Leu Leu Asn Leu Lys Ser Asn Gln Glu Leu 110 115 120 125			387
tcc gaa caa ggg aca tct ttt tca cag act tgc ctt aca cag ttt ctt Ser Glu Gln Gly Thr Ser Phe Ser Gln Thr Cys Leu Thr Gln Phe Leu 130 135 140			435
gaa gac gag tac cca gac atg ccc act gaa ggc ata aaa aat ctt gtt Glu Asp Glu Tyr Pro Asp Met Pro Thr Glu Gly Ile Lys Asn Leu Val 145 150 155			483
gac ttt ctc act ggt gag gaa gtc gtg tgt cac gtg gct aga aac ttg Asp Phe Leu Thr Gly Glu Glu Val Val Cys His Val Ala Arg Asn Leu 160 165 170			531
gct gtg gag cag tta aca ctg agt gaa gaa ttc cca gtg ccc cca gct Ala Val Glu Gln Leu Thr Leu Ser Glu Glu Phe Pro Val Pro Pro Ala 175 180 185			579
gtg tta cag cag act ttc ttt gca gtt att gga gcc ctg tta cag agc Val Leu Gln Gln Thr Phe Phe Ala Val Ile Gly Ala Leu Leu Gln Ser 190 195 200 205			627
agt gga cct gag agg act gca ctt ttc atc agg gac ttc tta att act Ser Gly Pro Glu Arg Thr Ala Leu Phe Ile Arg Asp Phe Leu Ile Thr 210 215 220			675
caa atg act gga aaa gag ctc ttt gag atg tgg aag ata ata aat ccc Gln Met Thr Gly Lys Glu Leu Phe Glu Met Trp Lys Ile Ile Asn Pro 225 230 235			723
atg ggg cta ttg gta gaa gaa ctg aag aaa agg aat gtt tca gct cct Met Gly Leu Leu Val Glu Glu Leu Lys Lys Arg Asn Val Ser Ala Pro 240 245 250			771
gaa tca aga ctt act agg cag tct ggt ggc acc aca gct ttg cct ttg Glu Ser Arg Leu Thr Arg Gln Ser Gly Gly Thr Thr Ala Leu Pro Leu 255 260 265			819
tat ttt gtt ggc tta tac tgt gat aaa aag ttg att gca gaa gga cct Tyr Phe Val Gly Leu Tyr Cys Asp Lys Lys Leu Ile Ala Glu Gly Pro 270 275 280 285			867
ggg gaa aca gta ttg gtt gca gaa gaa gag gct gct cga gtg gcc ctt Gly Glu Thr Val Leu Val Ala Glu Glu Glu Ala Ala Arg Val Ala Leu 290 295 300			915
aga aaa ctt tat gga ttc aca gaa aat aga cgg ccg tgg aac tat tcc Arg Lys Leu Tyr Gly Phe Thr Glu Asn Arg Arg Pro Trp Asn Tyr Ser 305 310 315			963



				165				170					175		
Gln	Leu	Thr	Leu	Ser	Glu	Glu	Phe	Pro	Val	Pro	Pro	Ala	Val	Leu	Gln
			180					185					190		
Gln	Thr	Phe	Phe	Ala	Val	Ile	Gly	Ala	Leu	Leu	Gln	Ser	Ser	Gly	Pro
		195					200					205			
Glu	Arg	Thr	Ala	Leu	Phe	Ile	Arg	Asp	Phe	Leu	Ile	Thr	Gln	Met	Thr
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Gly	Lys	Glu	Leu	Phe	Glu	Met	Trp	Lys	Ile	Ile	Asn	Pro	Met	Gly	Leu
225					230					235					240
Leu	Val	Glu	Glu	Leu	Lys	Lys	Arg	Asn	Val	Ser	Ala	Pro	Glu	Ser	Arg
				245					250					255	
Leu	Thr	Arg	Gln	Ser	Gly	Gly	Thr	Thr	Ala	Leu	Pro	Leu	Tyr	Phe	Val
			260					265					270		
Gly	Leu	Tyr	Cys	Asp	Lys	Lys	Leu	Ile	Ala	Glu	Gly	Pro	Gly	Glu	Thr
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Val	Leu	Val	Ala	Glu	Glu	Glu	Ala	Ala	Arg	Val	Ala	Leu	Arg	Lys	Leu
	290					295					300				
Tyr	Gly	Phe	Thr	Glu	Asn	Arg	Arg	Pro	Trp	Asn	Tyr	Ser	Lys	Pro	Lys
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gccccggacc aggtgcctcc atg gca ggc tct gaa gag ctg ggg ctc cgg gaa 113  
Met Ala Gly Ser Glu Glu Leu Gly Leu Arg Glu  
1 5 10

gac acg ctg agg gtc cta gct gcc ttc ctt agg cgt ggt gag gct gcc 161  
Asp Thr Leu Arg Val Leu Ala Ala Phe Leu Arg Arg Gly Glu Ala Ala  
15 20 25

ggg tct cct gtt cca act cca cct aga agc cct gcc caa gaa gag cca 209  
Gly Ser Pro Val Pro Thr Pro Pro Arg Ser Pro Ala Gln Glu Glu Pro  
30 35 40

aca gac ttc ctg agc cgc ctt cga aga tgt ctt ccc tgc tcc ctg ggg 257  
Thr Asp Phe Leu Ser Arg Leu Arg Arg Cys Leu Pro Cys Ser Leu Gly  
45 50 55

cga gga gca gcc ccc tct gag tcc cct cgg cct tgc tct ctg ccc atc 305  
Arg Gly Ala Ala Pro Ser Glu Ser Pro Arg Pro Cys Ser Leu Pro Ile  
60 65 70 75

cgc ccc tgc tat ggt tta gag cct ggc cca gct act cca gac ttc tat 353  
Arg Pro Cys Tyr Gly Leu Glu Pro Gly Pro Ala Thr Pro Asp Phe Tyr

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gct ttg gtg gcc cag cgg ctg gaa cag ctg gtc caa gag cag ctg aaa			401
Ala Leu Val Ala Gln Arg Leu Glu Gln Leu Val Gln Glu Gln Leu Lys			
95	100	105	
tct ccg ccc agc cca gaa tta cag ggt ccc cca tcg aca gag aag gaa			449
Ser Pro Pro Ser Pro Glu Leu Gln Gly Pro Pro Ser Thr Glu Lys Glu			
110	115	120	
gcc ata ctg cgg agg ctg gtg gcc ctg ctg gag gag gag gca gaa gtc			497
Ala Ile Leu Arg Arg Leu Val Ala Leu Leu Glu Glu Glu Ala Glu Val			
125	130	135	
att aac cag aag gag ggc atc ctg gct gtt tca ccc gtg gac ttg aac			545
Ile Asn Gln Lys Glu Gly Ile Leu Ala Val Ser Pro Val Asp Leu Asn			
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Leu Pro Leu Asp			
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Arg Leu Arg Arg Cys Leu Pro Cys Ser Leu Gly Arg Gly Ala Ala Pro			
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Ser Glu Ser Pro Arg Pro Cys Ser Leu Pro Ile Arg Pro Cys Tyr Gly			
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Arg Leu Glu Gln Leu Val Gln Glu Gln Leu Lys Ser Pro Pro Ser Pro			
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Glu Leu Gln Gly Pro Pro Ser Thr Glu Lys Glu Ala Ile Leu Arg Arg			
115 120 125			
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tcgggaggaa ag atg aat ggg agg gct gat ttt cga gag ccg aat gca gag 171  
 Met Asn Gly Arg Ala Asp Phe Arg Glu Pro Asn Ala Glu  
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gtt cca aga cca att ccc cac ata ggg cct gat tac att cca aca gag 219  
 Val Pro Arg Pro Ile Pro His Ile Gly Pro Asp Tyr Ile Pro Thr Glu  
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gaa gaa agg aga gtc ttc gca gaa tgc aat gat gaa agc ttc tgg ttc 267  
 Glu Glu Arg Arg Val Phe Ala Glu Cys Asn Asp Glu Ser Phe Trp Phe  
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aga tct gtg cct ttg gct gca aca agt atg ttg att act caa gga tta 315  
 Arg Ser Val Pro Leu Ala Ala Thr Ser Met Leu Ile Thr Gln Gly Leu  
 50 55 60

att agt aaa gga ata ctt tca agt cat ccc aaa tat ggt tcc atc cct 363  
 Ile Ser Lys Gly Ile Leu Ser Ser His Pro Lys Tyr Gly Ser Ile Pro  
 65 70 75

aaa ctt ata ctt gct tgt atc atg gga tac ttt gct gga aaa ctt tct 411  
 Lys Leu Ile Leu Ala Cys Ile Met Gly Tyr Phe Ala Gly Lys Leu Ser  
 80 85 90

tat gtg aaa act tgc caa gag aaa ttc aag aaa ctt gaa aat tcc ccc 459  
 Tyr Val Lys Thr Cys Gln Glu Lys Phe Lys Lys Leu Glu Asn Ser Pro  
 95 100 105

ctt gga gaa gct tta cga tca gga caa gca cga cga tct tca cca cct 507  
 Leu Gly Glu Ala Leu Arg Ser Gly Gln Ala Arg Arg Ser Ser Pro Pro  
 110 115 120 125

ggg cac tat tat caa aag tca aaa tat gac tca agt gtg agt ggt caa 555  
 Gly His Tyr Tyr Gln Lys Ser Lys Tyr Asp Ser Ser Val Ser Gly Gln  
 130 135 140

tca tct ttt gtg aca tcc cca gca gca gac aac ata gaa atg ctt cct 603  
 Ser Ser Phe Val Thr Ser Pro Ala Ala Asp Asn Ile Glu Met Leu Pro  
 145 150 155

cat tat gag cca att cca ttc agt tct tct atg aat gaa tct gct ccc 651  
 His Tyr Glu Pro Ile Pro Phe Ser Ser Ser Met Asn Glu Ser Ala Pro  
 160 165 170





70 75 80

cgc cgc ttc ctg cag tgc gct gag cag gtg cag ccg cca cgc tca cct 466  
 Arg Arg Phe Leu Gln Cys Ala Glu Gln Val Gln Pro Pro Arg Ser Pro  
 85 90 95

gca act gtg gag gca cag cca ctt cct gcc tcc tga ggactcctct 512  
 Ala Thr Val Glu Ala Gln Pro Leu Pro Ala Ser  
 100 105 110

gacggcagga aaactggaca tgaatgactg cccccccgcc cctccctgc agagtggcca 572

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			20					25					30		
Asp	Cys	His	Tyr	Leu	Lys	Met	Ser	Ile	Ala	Gln	Cys	Thr	Ser	Ser	His
		35					40					45			
Pro	Ile	Ile	Arg	Gln	Ile	Arg	Gln	Ala	Cys	Ala	Gln	Pro	Phe	Glu	Ala
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Phe	Glu	Glu	Cys	Leu	Arg	Gln	Asn	Glu	Ala	Ala	Val	Gly	Asn	Cys	Ala
	65				70				75						80
Glu	His	Met	Arg	Arg	Phe	Leu	Gln	Cys	Ala	Glu	Gln	Val	Gln	Pro	Pro
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 <222> (40)..(411)

<400> 115

gcggaagtac ggaccgtgaa ctggagtgga atcgcgact atg gga gct ccg ggg 54  
 Met Gly Ala Pro Gly  
 1 5

gga aag atc aac cgg ccc cga acg gag ctg aag aag aag ctg ttc aaa 102  
 Gly Lys Ile Asn Arg Pro Arg Thr Glu Leu Lys Lys Lys Leu Phe Lys  
 10 15 20

cgc cgg cgg gtg ttg aat cgg gag cgg cgt ctg agg cac cgg gtg gtc 150  
Arg Arg Arg Val Leu Asn Arg Glu Arg Arg Leu Arg His Arg Val Val  
25 30 35

ggg gct gtg ata gac caa ggg ctg atc acg cgg cac cac ctc aag aag 198  
Gly Ala Val Ile Asp Gln Gly Leu Ile Thr Arg His His Leu Lys Lys  
40 45 50

cgg gcg tcc agt gca cgt gcc aac att aca ctg tca ggg aag aag cgc 246  
Arg Ala Ser Ser Ala Arg Ala Asn Ile Thr Leu Ser Gly Lys Lys Arg  
55 60 65

aga aaa ctc ctc cag cag atc cgg ctt gcc cag aaa gag aag aca gcc 294  
Arg Lys Leu Leu Gln Gln Ile Arg Leu Ala Gln Lys Glu Lys Thr Ala  
70 75 80 85

atg gaa gtg gaa gcc cct tca aag cca gcc agg act agt gaa cca cag 342  
Met Glu Val Glu Ala Pro Ser Lys Pro Ala Arg Thr Ser Glu Pro Gln  
90 95 100

ctc aaa agg caa aag aag aca aaa gcc ccc cag gat gta gaa atg aag 390  
Leu Lys Arg Gln Lys Lys Thr Lys Ala Pro Gln Asp Val Glu Met Lys  
105 110 115

gac ctt gaa gat gag agc taa acctcttcca ctagaagatt ctcaactgga 441  
Asp Leu Glu Asp Glu Ser  
120

gccagccttc agactcagtg gttgtttcag aggactttga caaaagcaag gcccttttc 501

actctccaga tttcctccta cctaattggcc tactgacctc ccctagaggg atgtcttttg 561

gaggggaagaa ggtacagaag aaagattgga gaagggtctc tctagcagtc aactccattt 621

gtaataaagc cctagcactc tg 643

<210> 116

<211> 123

<212> PRT

<213> Homo sapiens

<400> 116

Met Gly Ala Pro Gly Gly Lys Ile Asn Arg Pro Arg Thr Glu Leu Lys  
1 5 10 15  
Lys Lys Leu Phe Lys Arg Arg Arg Val Leu Asn Arg Glu Arg Arg Leu  
20 25 30  
Arg His Arg Val Val Gly Ala Val Ile Asp Gln Gly Leu Ile Thr Arg  
35 40 45  
His His Leu Lys Lys Arg Ala Ser Ser Ala Arg Ala Asn Ile Thr Leu  
50 55 60  
Ser Gly Lys Lys Arg Arg Lys Leu Leu Gln Gln Ile Arg Leu Ala Gln  
65 70 75 80  
Lys Glu Lys Thr Ala Met Glu Val Glu Ala Pro Ser Lys Pro Ala Arg  
85 90 95  
Thr Ser Glu Pro Gln Leu Lys Arg Gln Lys Lys Thr Lys Ala Pro Gln  
100 105 110

Asp Val Glu Met Lys Asp Leu Glu Asp Glu Ser  
115 120

<210> 117  
<211> 1293  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (306)..(1019)

<400> 117  
g t t a g g c t g a g c c t c t t g c t t g c t g t g a c t g g t g g a g c t g c c g c g c t g t c c g c g t t a t c t 60  
c c t c c c g g t g a g a a c g a a c c g c a g t g t c c a c c g g c g a g g a g c c a g c c c t g t c c c g g t c a g 120  
a g a a a g a c g a c g a g g a t a c c t g g g a g c g g g c g g c g g c c g g g c t g g g c c g c g c c g g t g c g g 180  
g c t g g c g a c t c t g c t c c t c c g c t t g c t g c t g t c t c t g g g a a c t g g g t g c c a g c g t g a g g 240  
g g c t t c c a g c g g a c a g g a c c c c c t t c c c c g g c t c c c c t g c c c a c c c t g c g g g g a g g g c 300  
g g a a g a t g c c g g t g a a g a a g a a g a g a a a t c c c t g g g g t g g a g a g a g a 350  
Met Pro Val Lys Lys Lys Arg Lys Ser Pro Gly Val Ala Ala Ala  
1 5 10 15  
g t a g c g g a a g a c g g a g g c c t c a a a a a g t g t a a a a t c t c c a g c t a t t g c 398  
Val Ala Glu Asp Gly Gly Leu Lys Lys Cys Lys Ile Ser Ser Tyr Cys  
20 25 30  
a g a t c c c a a c c c c t g c t a g a c t a a t a g t g g a g a g g a a c a t t t t t c a 446  
Arg Ser Gln Pro Pro Ala Arg Leu Ile Ser Gly Glu Glu His Phe Ser  
35 40 45  
a g c a a g a a g t g c c t g g t t g g t t t t a t g a a t a t g c a g g t c c t g a t g a a 494  
Ser Lys Lys Cys Leu Ala Trp Phe Tyr Glu Tyr Ala Gly Pro Asp Glu  
50 55 60  
g t t g t a g g g c c a g a a g g a a t g g a a a t t t t g t g a a g a c a t t g g t g t t 542  
Val Val Gly Pro Glu Gly Met Glu Lys Phe Cys Glu Asp Ile Gly Val  
65 70 75  
g a a c c t g a a a a t a t t a t t a t g t t a g t t a g c g t g g a a a t t g g a g g c t 590  
Glu Pro Glu Asn Ile Ile Met Leu Val Leu Ala Trp Lys Leu Glu Ala  
80 85 90 95  
g a a a g c a t g g g a t t t t t a c c a a g g a a g a a t g g t t a a a g g a a t g a c t 638  
Glu Ser Met Gly Phe Phe Thr Lys Glu Glu Trp Leu Lys Gly Met Thr  
100 105 110  
t c a t t a c a g t g t g a c t g c a c a g a a g t t a c a a a c a a a t t t g a c t t t 686  
Ser Leu Gln Cys Asp Cys Thr Glu Lys Leu Gln Asn Lys Phe Asp Phe  
115 120 125  
t t g c g c t c a c a g t t g a a t g a t a t t c g t c a t t t a a g a a t a t c t a c a g a 734

Leu Arg Ser Gln Leu Asn Asp Ile Ser Ser Phe Lys Asn Ile Tyr Arg  
 130 135 140

tat gcc ttt gat ttt gca agg gat aaa gat cag aga agc ctt gat att 782  
 Tyr Ala Phe Asp Phe Ala Arg Asp Lys Asp Gln Arg Ser Leu Asp Ile  
 145 150 155

gat act gct aaa tct atg tta gct ctt ctg ctt ggg agg aca tgg cca 830  
 Asp Thr Ala Lys Ser Met Leu Ala Leu Leu Leu Gly Arg Thr Trp Pro  
 160 165 170 175

ctg ttt tca gta ttt tac cag tac ctg gag caa tca aag tat cgt gtt 878  
 Leu Phe Ser Val Phe Tyr Gln Tyr Leu Glu Gln Ser Lys Tyr Arg Val  
 180 185 190

atg aac aaa gat caa tgg tac aat gta tta gaa ttc agc aga aca gtc 926  
 Met Asn Lys Asp Gln Trp Tyr Asn Val Leu Glu Phe Ser Arg Thr Val  
 195 200 205

cat gct gat ctt agt aac tat gat gaa gat ggt gct tgg cct gtt ctt 974  
 His Ala Asp Leu Ser Asn Tyr Asp Glu Asp Gly Ala Trp Pro Val Leu  
 210 215 220

ctt gat gaa ttt gtt gag tgg caa aaa gtc cgt cag aca tca tag 1019  
 Leu Asp Glu Phe Val Glu Trp Gln Lys Val Arg Gln Thr Ser  
 225 230 235

caagaactat gtgaagaaaa tgcaaaccctt tcaattccca cgtgtataca agctaattgtg 1079

atgaggggga aaaaaatcca acgggtgcat tttcattcat atgaaagact tctcatagta 1139

cttttttttc ctttttttaa aggaggtttt tcttggtaca tgtgatgggc attgagccac 1199

acctcttctt agactgaata ttgaagtttt tgttttgagt tatgtttata acattttattt 1259

cagaacaata aagattcaga tttgtgacaa aggc 1293

<210> 118  
 <211> 237  
 <212> PRT  
 <213> Homo sapiens

<400> 118  
 Met Pro Val Lys Lys Lys Arg Lys Ser Pro Gly Val Ala Ala Ala Val  
 1 5 10 15  
 Ala Glu Asp Gly Gly Leu Lys Lys Cys Lys Ile Ser Ser Tyr Cys Arg  
 20 25 30  
 Ser Gln Pro Pro Ala Arg Leu Ile Ser Gly Glu Glu His Phe Ser Ser  
 35 40 45  
 Lys Lys Cys Leu Ala Trp Phe Tyr Glu Tyr Ala Gly Pro Asp Glu Val  
 50 55 60  
 Val Gly Pro Glu Gly Met Glu Lys Phe Cys Glu Asp Ile Gly Val Glu  
 65 70 75 80  
 Pro Glu Asn Ile Ile Met Leu Val Leu Ala Trp Lys Leu Glu Ala Glu  
 85 90 95  
 Ser Met Gly Phe Phe Thr Lys Glu Glu Trp Leu Lys Gly Met Thr Ser



acc cac ccc gga gac ccc cgc ttc cag tgc agt ctc tgg cat ctc tat 462  
 Thr His Pro Gly Asp Pro Arg Phe Gln Cys Ser Leu Trp His Leu Tyr  
 90 95 100 105

ccc cta tga ggcaccacgt aagacctcct gcccttagct ctcttgctca 511  
 Pro Leu

ccaccaaga acctcaggac agaagcgaga gccattgct cctgctcagc tcagcccggc 571

tgcgaggagaa cccttggcag gcagaacctg gaggtgtcag aggctcaact cctccatcta 631

accagcaggc tcccagagtc cccggaagag cctgctcagc tgaagcagag tgcttctaga 691

tgagagtggt tctactgggga aaaggacctg gccatcacct tccaatacct gctgcctgtc 751

tccctgaccc atgatctggc aagttaggca cagtcagaca tggacagttg atccatgagg 811

aaaagatgct ctccaccta aggccaggaa tctgagagca ggactggctg agctcccagg 871

gcaaggggtt cactaatgct tatcaataaa gaatattgag cctgg 916

<210> 120  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

<400> 120  
 Met Gly Arg Lys Arg Leu Ile Thr Asp Ser Tyr Pro Val Val Lys Arg  
 1 5 10 15  
 Arg Glu Gly Pro Ala Gly His Ser Lys Gly Glu Leu Ala Pro Glu Leu  
 20 25 30  
 Gly Glu Glu Pro Gln Pro Arg Asp Glu Glu Glu Ala Glu Leu Glu Leu  
 35 40 45  
 Leu Arg Gln Phe Asp Leu Ala Trp Gln Tyr Gly Pro Cys Thr Gly Ile  
 50 55 60  
 Thr Arg Leu Gln Arg Trp Cys Arg Ala Lys Gln Met Gly Leu Glu Pro  
 65 70 75 80  
 Pro Pro Glu Val Trp Gln Val Leu Lys Thr His Pro Gly Asp Pro Arg  
 85 90 95  
 Phe Gln Cys Ser Leu Trp His Leu Tyr Pro Leu  
 100 105

<210> 121  
 <211> 1002  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (51)..(731)

<400> 121  
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 Met Arg

cag aag cac tac ctt gag gct gca gcg cgg gga ctg cac gac agc tgc	104
Gln Lys His Tyr Leu Glu Ala Ala Ala Arg Gly Leu His Asp Ser Cys	
5 10 15	
ccg ggc caa gcc cgc tac ctc ctt ctc ttt ctc ttt tac agc tgg gcc	152
Pro Gly Gln Ala Arg Tyr Leu Leu Leu Phe Leu Phe Tyr Ser Trp Ala	
20 25 30	
tac act tcg tcg cac gat gat aag agc act ttt gaa gaa acg tgt cca	200
Tyr Thr Ser Ser His Asp Asp Lys Ser Thr Phe Glu Glu Thr Cys Pro	
35 40 45 50	
tac tgt ttc cag ctg ttg gtt ctg gat aac tct cga gtg cgt ctc aaa	248
Tyr Cys Phe Gln Leu Val Leu Asp Asn Ser Arg Val Arg Leu Lys	
55 60 65	
ccc aaa gcc agg ttg aca ccc aaa ata cag aaa ctt ctt aat cga gaa	296
Pro Lys Ala Arg Leu Thr Pro Lys Ile Gln Lys Leu Leu Asn Arg Glu	
70 75 80	
gcg aga aac tat aca ctc agt ttt aaa gaa gca aaa atg gtg aaa aag	344
Ala Arg Asn Tyr Thr Leu Ser Phe Lys Glu Ala Lys Met Val Lys Lys	
85 90 95	
ttc aaa gac tcc aaa agt gta ttg ttg atc act tgt aaa aca tgc aac	392
Phe Lys Asp Ser Lys Ser Val Leu Leu Ile Thr Cys Lys Thr Cys Asn	
100 105 110	
aga aca gtg aaa cat cat ggt aaa agt aga agc ttt gtg tca aca ttg	440
Arg Thr Val Lys His His Gly Lys Ser Arg Ser Phe Val Ser Thr Leu	
115 120 125 130	
aag agc aat cct gcc act cct aca agt aaa ctc agc ctg aag aca cca	488
Lys Ser Asn Pro Ala Thr Pro Thr Ser Lys Leu Ser Leu Lys Thr Pro	
135 140 145	
gag aga agg act gca aac cca aat cat gac atg tct ggc tcg aaa ggc	536
Glu Arg Arg Thr Ala Asn Pro Asn His Asp Met Ser Gly Ser Lys Gly	
150 155 160	
aag agc cca gca tcg gtt ttc aga aca cct aca tct gga cag tca gta	584
Lys Ser Pro Ala Ser Val Phe Arg Thr Pro Thr Ser Gly Gln Ser Val	
165 170 175	
tct act tgc tcc tca aag aac acc agc aaa aca aag aaa cac ttc tct	632
Ser Thr Cys Ser Ser Lys Asn Thr Ser Lys Thr Lys Lys His Phe Ser	
180 185 190	
caa cta aaa atg tta ctt agt cag aat gaa tcc caa aag att cca aag	680
Gln Leu Lys Met Leu Leu Ser Gln Asn Glu Ser Gln Lys Ile Pro Lys	
195 200 205 210	
gtg gac ttc aga aat ttc tta tct tct ctg aag ggt gga ctt tta aaa	728
Val Asp Phe Arg Asn Phe Leu Ser Ser Leu Lys Gly Gly Leu Leu Lys	
215 220 225	

taa gaaatgcctg atgtcaattc tgaaactaaa gttggtaaaa caacttttta 781

aactcttatt ctttttttga atacatggaa actagatctg aatgcaaact tttcttggca 841

tccttcagtg tttatgggga aaatacctca ttagtgtgaa tacctgaaac ctgcctacct 901

cataggacag ctgtgaggat caaaaaatat atgaaagttc cttgtagata catatctata 961

gatatatatg tgtatgtata taaagataga tatatacatt g 1002

<210> 122  
 <211> 226  
 <212> PRT  
 <213> Homo sapiens

<400> 122

Met	Arg	Gln	Lys	His	Tyr	Leu	Glu	Ala	Ala	Ala	Arg	Gly	Leu	His	Asp
1				5					10					15	
Ser	Cys	Pro	Gly	Gln	Ala	Arg	Tyr	Leu	Leu	Leu	Phe	Leu	Phe	Tyr	Ser
			20					25					30		
Trp	Ala	Tyr	Thr	Ser	Ser	His	Asp	Asp	Lys	Ser	Thr	Phe	Glu	Glu	Thr
			35				40					45			
Cys	Pro	Tyr	Cys	Phe	Gln	Leu	Leu	Val	Leu	Asp	Asn	Ser	Arg	Val	Arg
	50					55				60					
Leu	Lys	Pro	Lys	Ala	Arg	Leu	Thr	Pro	Lys	Ile	Gln	Lys	Leu	Leu	Asn
65					70					75					80
Arg	Glu	Ala	Arg	Asn	Tyr	Thr	Leu	Ser	Phe	Lys	Glu	Ala	Lys	Met	Val
				85					90					95	
Lys	Lys	Phe	Lys	Asp	Ser	Lys	Ser	Val	Leu	Leu	Ile	Thr	Cys	Lys	Thr
			100					105					110		
Cys	Asn	Arg	Thr	Val	Lys	His	His	Gly	Lys	Ser	Arg	Ser	Phe	Val	Ser
	115						120					125			
Thr	Leu	Lys	Ser	Asn	Pro	Ala	Thr	Pro	Thr	Ser	Lys	Leu	Ser	Leu	Lys
130						135					140				
Thr	Pro	Glu	Arg	Arg	Thr	Ala	Asn	Pro	Asn	His	Asp	Met	Ser	Gly	Ser
145					150					155				160	
Lys	Gly	Lys	Ser	Pro	Ala	Ser	Val	Phe	Arg	Thr	Pro	Thr	Ser	Gly	Gln
				165				170						175	
Ser	Val	Ser	Thr	Cys	Ser	Ser	Lys	Asn	Thr	Ser	Lys	Thr	Lys	Lys	His
		180					185					190			
Phe	Ser	Gln	Leu	Lys	Met	Leu	Leu	Ser	Gln	Asn	Glu	Ser	Gln	Lys	Ile
	195					200					205				
Pro	Lys	Val	Asp	Phe	Arg	Asn	Phe	Leu	Ser	Ser	Leu	Lys	Gly	Gly	Leu
210						215					220				
Leu	Lys														
225															

<210> 123  
 <211> 1753  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> CDS

<222> (268)..(1455)

<400> 123

gcctttgtttt acaaccctgc catgatctcc ctcttgcaaa agcgagggct acagaacagg 60

cattcaggag tcoctgtgctc cagtcacagc cttttctgtt cttcagctag gagacaccaa 120

accctcagga agatttacta tagctaagag aaaactgcag cagaaagggc gcggctacct 180

acttcttaaa ttccgtttgt ggaccctcag actcttagtc ccctactccc agatacagcg 240

gccctaccgt ggctcctggc aagaagc atg gat ctc gga atc cct gac ctg ctg 294

Met Asp Leu Gly Ile Pro Asp Leu Leu

1

5

gac gcg tgg ctg gag ccc cca gag gat atc ttc tcg aca gga tcc gtc 342

Asp Ala Trp Leu Glu Pro Pro Glu Asp Ile Phe Ser Thr Gly Ser Val

10

15

20

25

ctg gag ctg gga ctc cac tgc ccc cct cca gag gtt ccg gta act agg 390

Leu Glu Leu Gly Leu His Cys Pro Pro Pro Glu Val Pro Val Thr Arg

30

35

40

cta cag gaa cag gga ctg caa ggc tgg aag tcc ggt ggg gac cgt ggc 438

Leu Gln Glu Gln Gly Leu Gln Gly Trp Lys Ser Gly Gly Asp Arg Gly

45

50

55

tgt ggc ctt caa gag agt gag cct gaa gat ttc ttg aag ctt ttc att 486

Cys Gly Leu Gln Glu Ser Glu Pro Glu Asp Phe Leu Lys Leu Phe Ile

60

65

70

gat ccc aat gag gtg tac tgc tca gaa gca tct cct ggc agt gac agt 534

Asp Pro Asn Glu Val Tyr Cys Ser Glu Ala Ser Pro Gly Ser Asp Ser

75

80

85

ggc atc tct gag gac ccc tgc cat cca gac agt ccc cct gcc ccc agg 582

Gly Ile Ser Glu Asp Pro Cys His Pro Asp Ser Pro Pro Ala Pro Arg

90

95

100

105

gca acc agt tct cct atg ctc tat gag gtt gtc tat gag gca ggg gcc 630

Ala Thr Ser Ser Pro Met Leu Tyr Glu Val Val Tyr Glu Ala Gly Ala

110

115

120

ctg gag agg atg cag ggg gaa act ggg cca aat gta ggc ctt atc tcc 678

Leu Glu Arg Met Gln Gly Glu Thr Gly Pro Asn Val Gly Leu Ile Ser

125

130

135

atc cag cta gat cag tgg agc cca gca ttt atg gtg cct gat tcc tgc 726

Ile Gln Leu Asp Gln Trp Ser Pro Ala Phe Met Val Pro Asp Ser Cys

140

145

150

atg gtc agt gag ctg ccc ttt gat gct cat gcc cac atc ctg ccc aga 774

Met Val Ser Glu Leu Pro Phe Asp Ala His Ala His Ile Leu Pro Arg

155

160

165

gca ggc acc gta gcc cca gtg ccc tgt aca acc ctg ctg ccc tgt caa 822

Ala 170	Gly	Thr	Val	Ala	Pro 175	Val	Pro	Cys	Thr	Thr 180	Leu	Leu	Pro	Cys	Gln 185	
acc Thr	ctg Leu	ttc Phe	ctg Leu	acc Thr	gat Asp	gag Glu	gag Glu	aag Lys	cgt Arg	ctg Leu	ctg Leu	ggg Gly	cag Gln	gaa Glu	ggg Gly	870
				190					195					200		
gtt Val	tcc Ser	ctg Leu	ccc Pro	tct Ser	cac His	ctg Leu	ccc Pro	ctc Leu	acc Thr	aag Lys	gca Ala	gag Glu	gag Glu	agg Arg	gtc Val	918
			205					210					215			
ctc Leu	aag Lys	aag Lys	gtc Val	agg Arg	agg Arg	aaa Lys	atc Ile	cgt Arg	aac Asn	aag Lys	cag Gln	tca Ser	gct Ala	cag Gln	gac Asp	966
		220					225					230				
agt Ser	cgg Arg	cgg Arg	cgg Arg	aag Lys	aag Lys	gag Glu	tac Tyr	att Ile	gat Asp	ggg Gly	ctg Leu	gag Glu	agc Ser	agg Arg	gtg Val	1014
	235					240					245					
gca Ala	gcc Ala	tgt Cys	tct Ser	gca Ala	cag Gln	aac Asn	caa Gln	gaa Glu	tta Leu	cag Gln	aaa Lys	aaa Lys	gtc Val	cag Gln	gag Glu	1062
250					255					260						265
ctg Leu	gag Glu	agg Arg	cac His	aac Asn	atc Ile	tcc Ser	ttg Leu	gta Val	gct Ala	cag Gln	ctc Leu	cgc Arg	cag Gln	ctg Leu	cag Gln	1110
				270					275					280		
acg Thr	cta Leu	att Ile	gct Ala	caa Gln	act Thr	tcc Ser	aac Asn	aaa Lys	gct Ala	gcc Ala	cag Gln	acc Thr	agc Ser	act Thr	tgt Cys	1158
			285					290					295			
gtt Val	ttg Leu	att Ile	ctt Leu	ctt Leu	ttt Phe	tcc Ser	ctg Leu	gct Ala	ctc Leu	atc Ile	atc Ile	ctg Leu	ccc Pro	agc Ser	ttc Phe	1206
		300					305					310				
agt Ser	cca Pro	ttc Phe	cag Gln	agt Ser	cga Arg	cca Pro	gaa Glu	gct Ala	ggg Gly	tct Ser	gag Glu	gat Asp	tac Tyr	cag Gln	cct Pro	1254
	315					320					325					
cac His	gga Gly	gtg Val	act Thr	tcc Ser	aga Arg	aat Asn	atc Ile	ctg Leu	acc Thr	cac His	aag Lys	gac Asp	gta Val	aca Thr	gaa Glu	1302
330					335					340						345
aat Asn	ctg Leu	gag Glu	acc Thr	caa Gln	gtg Val	gta Val	gag Glu	tcc Ser	aga Arg	ctg Leu	agg Arg	gag Glu	cca Pro	cct Pro	gga Gly	1350
				350					355					360		
gcc Ala	aag Lys	gat Asp	gca Ala	aat Asn	ggc Gly	tca Ser	aca Thr	agg Arg	aca Thr	ctg Leu	ctt Leu	gag Glu	aag Lys	atg Met	gga Gly	1398
			365					370					375			
ggg Gly	aag Lys	cca Pro	aga Arg	ccc Pro	agt Ser	ggg Gly	cgc Arg	atc Ile	cgg Arg	tcc Ser	gtg Val	ctg Leu	cat His	gca Ala	gat Asp	1446
		380					385					390				
gag Glu	atg Met	tga	gctggaacag				accttcctgg			cccacttcct			gatcacaagg			1495

aatcctgggc ttccttatgg ctttgcttcc cactgggatt cctacttagg tgtctgccct 1555  
 caggggtcca aatcaacttca ggacacccca agagatgtcc tttagtctct gcctgaggcc 1615  
 tagtctgcat ttgtttgcat atatgagagg gtacctcaaa tacttctgtt atgtatctgt 1675  
 gattttatatt cttctttggg tatagggttg aggggaaata agttttgagt gagaaataaa 1735  
 cgttttagct gaaattgt 1753

&lt;210&gt; 124

&lt;211&gt; 395

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 124

Met	Asp	Leu	Gly	Ile	Pro	Asp	Leu	Leu	Asp	Ala	Trp	Leu	Glu	Pro	Pro
1				5					10					15	
Glu	Asp	Ile	Phe	Ser	Thr	Gly	Ser	Val	Leu	Glu	Leu	Gly	Leu	His	Cys
		20					25					30			
Pro	Pro	Pro	Glu	Val	Pro	Val	Thr	Arg	Leu	Gln	Glu	Gln	Gly	Leu	Gln
		35				40					45				
Gly	Trp	Lys	Ser	Gly	Gly	Asp	Arg	Gly	Cys	Gly	Leu	Gln	Glu	Ser	Glu
	50				55				60						
Pro	Glu	Asp	Phe	Leu	Lys	Leu	Phe	Ile	Asp	Pro	Asn	Glu	Val	Tyr	Cys
65				70				75						80	
Ser	Glu	Ala	Ser	Pro	Gly	Ser	Asp	Ser	Gly	Ile	Ser	Glu	Asp	Pro	Cys
			85					90					95		
His	Pro	Asp	Ser	Pro	Pro	Ala	Pro	Arg	Ala	Thr	Ser	Ser	Pro	Met	Leu
		100					105						110		
Tyr	Glu	Val	Val	Tyr	Glu	Ala	Gly	Ala	Leu	Glu	Arg	Met	Gln	Gly	Glu
	115					120						125			
Thr	Gly	Pro	Asn	Val	Gly	Leu	Ile	Ser	Ile	Gln	Leu	Asp	Gln	Trp	Ser
	130				135					140					
Pro	Ala	Phe	Met	Val	Pro	Asp	Ser	Cys	Met	Val	Ser	Glu	Leu	Pro	Phe
145				150				155						160	
Asp	Ala	His	Ala	His	Ile	Leu	Pro	Arg	Ala	Gly	Thr	Val	Ala	Pro	Val
		165				170							175		
Pro	Cys	Thr	Thr	Leu	Leu	Pro	Cys	Gln	Thr	Leu	Phe	Leu	Thr	Asp	Glu
	180					185						190			
Glu	Lys	Arg	Leu	Leu	Gly	Gln	Glu	Gly	Val	Ser	Leu	Pro	Ser	His	Leu
	195				200						205				
Pro	Leu	Thr	Lys	Ala	Glu	Glu	Arg	Val	Leu	Lys	Lys	Val	Arg	Arg	Lys
	210				215					220					
Ile	Arg	Asn	Lys	Gln	Ser	Ala	Gln	Asp	Ser	Arg	Arg	Arg	Lys	Lys	Glu
225			230					235						240	
Tyr	Ile	Asp	Gly	Leu	Glu	Ser	Arg	Val	Ala	Ala	Cys	Ser	Ala	Gln	Asn
		245						250					255		
Gln	Glu	Leu	Gln	Lys	Lys	Val	Gln	Glu	Leu	Glu	Arg	His	Asn	Ile	Ser
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Leu	Val	Ala	Gln	Leu	Arg	Gln	Leu	Gln	Thr	Leu	Ile	Ala	Gln	Thr	Ser
	275					280						285			
Asn	Lys	Ala	Ala	Gln	Thr	Ser	Thr	Cys	Val	Leu	Ile	Leu	Leu	Phe	Ser
	290					295				300					

Leu Ala Leu Ile Ile Leu Pro Ser Phe Ser Pro Phe Gln Ser Arg Pro  
 305 310 315 320  
 Glu Ala Gly Ser Glu Asp Tyr Gln Pro His Gly Val Thr Ser Arg Asn  
 325 330 335  
 Ile Leu Thr His Lys Asp Val Thr Glu Asn Leu Glu Thr Gln Val Val  
 340 345 350  
 Glu Ser Arg Leu Arg Glu Pro Pro Gly Ala Lys Asp Ala Asn Gly Ser  
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 Ala Pro Gly Cys Gly Arg Val Val Ser His Ala Gly Ala Pro Gly Gly  
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 Gly Thr Arg Pro Pro  
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 gtagactgct gctagctgaa taccatctgg gagcataaag gtgacctgaa ggatgtcctt 512  
 ggtgaggatt ttgaaaattt gatcttcaca agagttgcct ggatcatttg aaatttctgg 572  
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 tgaggatgtg aataaatata ttaatgcaaa aaaaac 668

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Ile Leu Gln Arg Val Pro Gly Lys Gln Arg Phe Gly Ile Tyr Arg Phe  
10 15 20 25  
  
ctg ccc ttc ttt ttt gtc ctg gga gga acg atg gag tgg atc atg att 149  
Leu Pro Phe Phe Phe Val Leu Gly Gly Thr Met Glu Trp Ile Met Ile  
30 35 40  
  
aaa gtg cgc gtg ggc cag gag acc ttc tat gat gtc tac cgt aga aaa 197  
Lys Val Arg Val Gly Gln Glu Thr Phe Tyr Asp Val Tyr Arg Arg Lys  
45 50 55  
  
gcc tca gaa aga cag tat cag aga agg ctg gaa gat gaa tga 239  
Ala Ser Glu Arg Gln Tyr Gln Arg Arg Leu Glu Asp Glu  
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Lys Gln Arg Phe Gly Ile Tyr Arg Phe Leu Pro Phe Phe Phe Val Leu  
20 25 30  
Gly Gly Thr Met Glu Trp Ile Met Ile Lys Val Arg Val Gly Gln Glu  
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Met Glu Glu Lys Pro Gly Gln Pro  
1 5  
cag cct cag cac cat cac agc cac cac cat ccg cac cat cac cct cag 162  
Gln Pro Gln His His His Ser His His His Pro His His His Pro Gln  
10 15 20  
cag cag cag cag cag ccg cac cac cac cac cat tat tat ttc tac aac 210  
Gln Gln Gln Gln Gln Pro His His His His His Tyr Tyr Phe Tyr Asn  
25 30 35 40  
cac agc cac aac cac cac cac cac cat cat cac cag cag cct cac caa 258  
His Ser His Asn His His His His His His Gln Gln Pro His Gln  
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Tyr Leu Gln His Gly Ala Glu Gly Ser Pro Lys Ala Gln Pro Lys Pro  
60 65 70  
ctg aaa cat gag cag aaa cac acc ctc cag cag cac cag gaa acg ccg 354  
Leu Lys His Glu Gln Lys His Thr Leu Gln Gln His Gln Glu Thr Pro  
75 80 85  
aag aag aaa aca ggc tat ggt gaa cta aac ggt aat gct gga gaa aga 402  
Lys Lys Lys Thr Gly Tyr Gly Glu Leu Asn Gly Asn Ala Gly Glu Arg  
90 95 100  
gaa ata tct tta aag aac ctg agt tct gat gaa gcc acc aac cct att 450  
Glu Ile Ser Leu Lys Asn Leu Ser Ser Asp Glu Ala Thr Asn Pro Ile  
105 110 115 120  
tcc agg gtc ctc aat ggc aac cag caa gtt gta gac act agc ctg aag 498  
Ser Arg Val Leu Asn Gly Asn Gln Gln Val Val Asp Thr Ser Leu Lys  
125 130 135  
cag act gta aag gcc aac acc ttt ggg aaa gca gga att aaa acc aag 546  
Gln Thr Val Lys Ala Asn Thr Phe Gly Lys Ala Gly Ile Lys Thr Lys  
140 145 150  
aat ttc att cag aaa aac agt atg gac aaa aag aat ggg aag tct tat 594

Asn Phe Ile Gln Lys Asn Ser Met Asp Lys Lys Asn Gly Lys Ser Tyr	
155 160 165	
gaa aat aaa tct gga gag aat cag tct gta gat aag tct gat act ata	642
Glu Asn Lys Ser Gly Glu Asn Gln Ser Val Asp Lys Ser Asp Thr Ile	
170 175 180	
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Pro Ile Pro Asn Gly Val Val Thr Asn Asn Ser Gly Tyr Ile Thr Asn	
185 190 195 200	
ggt tat atg agt aaa gga gca gat aat gat ggt agt gga tct gag agc	738
Gly Tyr Met Ser Lys Gly Ala Asp Asn Asp Gly Ser Gly Ser Glu Ser	
205 210 215	
gga tat aca act cct aaa aaa agg aaa gct agg cgc aat agt gcc aag	786
Gly Tyr Thr Thr Pro Lys Lys Arg Lys Ala Arg Arg Asn Ser Ala Lys	
220 225 230	
ggt tgt gaa aac ctt aat ata gtg cag gac aaa ata atg caa caa gag	834
Gly Cys Glu Asn Leu Asn Ile Val Gln Asp Lys Ile Met Gln Gln Glu	
235 240 245	
acc agt gtc cca acc tta aaa cag gga ctt gaa act ttc aag cct gac	882
Thr Ser Val Pro Thr Leu Lys Gln Gly Leu Glu Thr Phe Lys Pro Asp	
250 255 260	
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Tyr Ser Glu Gln Lys Gly Asn Arg Val Asp Gly Ser Lys Pro Ile Trp	
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Lys Tyr Glu Thr Gly Pro Gly Gly Thr Ser Arg Gly Lys Pro Ala Val	
285 290 295	
ggt gat atg ctt cgg aaa agc tca gat agt aaa cct ggt gtg agc agc	1026
Gly Asp Met Leu Arg Lys Ser Ser Asp Ser Lys Pro Gly Val Ser Ser	
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aaa aag ttt gat gat cgg ccc aaa gga aag cat gct tca gct gtt gcc	1074
Lys Lys Phe Asp Asp Arg Pro Lys Gly Lys His Ala Ser Ala Val Ala	
315 320 325	
tcc aaa gag gac tcg tgg acc cta ttt aaa cca ccc cca gtt ttt cca	1122
Ser Lys Glu Asp Ser Trp Thr Leu Phe Lys Pro Pro Pro Val Phe Pro	
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Val Asp Asn Ser Ser Ala Lys Ile Val Pro Lys Ile Ser Tyr Ala Ser	
345 350 355 360	
aaa gtt aag gaa aac ctc aac aaa act ata cag aac tct tct gtg tca	1218
Lys Val Lys Glu Asn Leu Asn Lys Thr Ile Gln Asn Ser Ser Val Ser	
365 370 375	
cca act tca tct tca tca tct tca tca tct acc ggg gaa act cag acc	1266
Pro Thr Ser Ser Ser Ser Ser Ser Ser Ser Thr Gly Glu Thr Gln Thr	

380	385	390	
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gtt act tct gcc aac ttt tct aat ggg cct gtt tta gca ggg act gat Val Thr Ser Ala Asn Phe Ser Asn Gly Pro Val Leu Ala Gly Thr Asp 410 415 420			1362
gga aat gtt tat cct cca ggg ggt cag cca ctg cta act act gct gct Gly Asn Val Tyr Pro Pro Gly Gly Gln Pro Leu Leu Thr Thr Ala Ala 425 430 435 440			1410
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atg agt cta act tca gca gct gtt gaa caa att aag act agc ctt ttt Met Ser Leu Thr Ser Ala Ala Val Glu Gln Ile Lys Thr Ser Leu Phe 460 465 470			1506
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gat ctg ccc tct cag aca gat cag caa aac ctg ggg gat atc ttc cag Asp Leu Pro Ser Gln Thr Asp Gln Gln Asn Leu Gly Asp Ile Phe Gln 490 495 500			1602
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act gtt act ggg aag tca tca gag cat aaa gtg atg gag gtg aca ttt Thr Val Thr Gly Lys Ser Ser Glu His Lys Val Met Glu Val Thr Phe 525 530 535			1698
caa gga gaa tat cct gct act ttg gtt tca cag ggt gct gaa ata att Gln Gly Glu Tyr Pro Ala Thr Leu Val Ser Gln Gly Ala Glu Ile Ile 540 545 550			1746
ccc tca gga act gag cat cct gtg ttt ccc aag gct tac gag ctg gag Pro Ser Gly Thr Glu His Pro Val Phe Pro Lys Ala Tyr Glu Leu Glu 555 560 565			1794
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 620 625 630

act ttg tta ggc tct gcc aaa gaa cag aga tac cag aga ggc cta gaa 2034  
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 Arg Asn Asp Ser Trp Gly Ser Phe Asp Leu Arg Ala Ala Ile Val Tyr  
 650 655 660

cac act aaa gaa atg gaa tct att tgg aat ttg cag aag caa gat ccc 2130  
 His Thr Lys Glu Met Glu Ser Ile Trp Asn Leu Gln Lys Gln Asp Pro  
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aaa agg ata atc act tac aat gaa gcc atg gat agt cca gat caa tga 2178  
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acaaggcttt tatgctccta gatcttcaac gcagcagagg aaccataagt agaatacacag 2298

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<211> 695

<212> PRT

<213> Homo sapiens

<400> 130

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			20					25					30		
His	His	His	Tyr	Tyr	Phe	Tyr	Asn	His	Ser	His	Asn	His	His	His	His
			35				40					45			
His	His	His	Gln	Gln	Pro	His	Gln	Tyr	Leu	Gln	His	Gly	Ala	Glu	Gly
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Ser	Pro	Lys	Ala	Gln	Pro	Lys	Pro	Leu	Lys	His	Glu	Gln	Lys	His	Thr
65					70					75					80
Leu	Gln	Gln	His	Gln	Glu	Thr	Pro	Lys	Lys	Lys	Thr	Gly	Tyr	Gly	Glu
				85					90					95	
Leu	Asn	Gly	Asn	Ala	Gly	Glu	Arg	Glu	Ile	Ser	Leu	Lys	Asn	Leu	Ser
			100					105					110		
Ser	Asp	Glu	Ala	Thr	Asn	Pro	Ile	Ser	Arg	Val	Leu	Asn	Gly	Asn	Gln
			115				120						125		
Gln	Val	Val	Asp	Thr	Ser	Leu	Lys	Gln	Thr	Val	Lys	Ala	Asn	Thr	Phe
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Gly	Lys	Ala	Gly	Ile	Lys	Thr	Lys	Asn	Phe	Ile	Gln	Lys	Asn	Ser	Met
145					150				155						160
Asp	Lys	Lys	Asn	Gly	Lys	Ser	Tyr	Glu	Asn	Lys	Ser	Gly	Glu	Asn	Gln
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Ser	Val	Asp	Lys	Ser	Asp	Thr	Ile	Pro	Ile	Pro	Asn	Gly	Val	Val	Thr
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			210				215					220			
Lys	Ala	Arg	Arg	Asn	Ser	Ala	Lys	Gly	Cys	Glu	Asn	Leu	Asn	Ile	Val
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Gln	Asp	Lys	Ile	Met	Gln	Gln	Glu	Thr	Ser	Val	Pro	Thr	Leu	Lys	Gln
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			260					265					270		
Val	Asp	Gly	Ser	Lys	Pro	Ile	Trp	Lys	Tyr	Glu	Thr	Gly	Pro	Gly	Gly
			275				280						285		
Thr	Ser	Arg	Gly	Lys	Pro	Ala	Val	Gly	Asp	Met	Leu	Arg	Lys	Ser	Ser
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305					310					315					320
Gly	Lys	His	Ala	Ser	Ala	Val	Ala	Ser	Lys	Glu	Asp	Ser	Trp	Thr	Leu
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Phe	Lys	Pro	Pro	Pro	Val	Phe	Pro	Val	Asp	Asn	Ser	Ser	Ala	Lys	Ile
			340					345					350		
Val	Pro	Lys	Ile	Ser	Tyr	Ala	Ser	Lys	Val	Lys	Glu	Asn	Leu	Asn	Lys
			355				360						365		

Thr	Ile	Gln	Asn	Ser	Ser	Val	Ser	Pro	Thr	Ser	Ser	Ser	Ser	Ser	Ser	
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Ser	Ser	Thr	Gly	Glu	Thr	Gln	Thr	Gln	Ser	Ser	Ser	Arg	Leu	Ser	Gln	
385					390				395						400	
Val	Pro	Met	Ser	Ala	Leu	Lys	Ser	Val	Thr	Ser	Ala	Asn	Phe	Ser	Asn	
			405						410					415		
Gly	Pro	Val	Leu	Ala	Gly	Thr	Asp	Gly	Asn	Val	Tyr	Pro	Pro	Gly	Gly	
		420						425					430			
Gln	Pro	Leu	Leu	Thr	Thr	Ala	Ala	Asn	Thr	Leu	Thr	Pro	Ile	Ser	Ser	
		435				440						445				
Gly	Thr	Asp	Ser	Val	Leu	Gln	Asp	Met	Ser	Leu	Thr	Ser	Ala	Ala	Val	
450						455						460				
Glu	Gln	Ile	Lys	Thr	Ser	Leu	Phe	Ile	Tyr	Pro	Ser	Asn	Met	Gln	Thr	
465					470					475					480	
Met	Leu	Leu	Ser	Thr	Ala	Gln	Val	Asp	Leu	Pro	Ser	Gln	Thr	Asp	Gln	
			485						490					495		
Gln	Asn	Leu	Gly	Asp	Ile	Phe	Gln	Asn	Gln	Trp	Gly	Leu	Ser	Phe	Ile	
		500						505					510			
Asn	Glu	Pro	Ser	Ala	Gly	Pro	Glu	Thr	Val	Thr	Gly	Lys	Ser	Ser	Glu	
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His	Lys	Val	Met	Glu	Val	Thr	Phe	Gln	Gly	Glu	Tyr	Pro	Ala	Thr	Leu	
530						535						540				
Val	Ser	Gln	Gly	Ala	Glu	Ile	Ile	Pro	Ser	Gly	Thr	Glu	His	Pro	Val	
545					550					555					560	
Phe	Pro	Lys	Ala	Tyr	Glu	Leu	Glu	Lys	Arg	Thr	Ser	Pro	Gln	Val	Leu	
			565						570					575		
Gly	Ser	Ile	Leu	Lys	Ser	Gly	Thr	Thr	Ser	Glu	Ser	Gly	Ala	Leu	Ser	
		580						585					590			
Leu	Glu	Pro	Ser	His	Ile	Gly	Asp	Leu	Gln	Lys	Ala	Asp	Thr	Ser	Ser	
		595					600					605				
Gln	Gly	Ala	Leu	Val	Phe	Leu	Ser	Lys	Asp	Tyr	Glu	Ile	Glu	Ser	Gln	
610						615					620					
Asn	Pro	Leu	Ala	Ser	Pro	Thr	Asn	Thr	Leu	Leu	Gly	Ser	Ala	Lys	Glu	
625					630					635					640	
Gln	Arg	Tyr	Gln	Arg	Gly	Leu	Glu	Arg	Asn	Asp	Ser	Trp	Gly	Ser	Phe	
			645						650					655		
Asp	Leu	Arg	Ala	Ala	Ile	Val	Tyr	His	Thr	Lys	Glu	Met	Glu	Ser	Ile	
			660					665					670			
Trp	Asn	Leu	Gln	Lys	Gln	Asp	Pro	Lys	Arg	Ile	Ile	Thr	Tyr	Asn	Glu	
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690						695										

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 <212> DNA  
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 <222> (100)..(699)

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	Met	Ser	Asn	Met	Glu	
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Lys His Leu Phe Asn Leu Lys Phe Ala Ala Lys Glu Leu Ser Arg Ser						
	10			15	20	
gcc aaa aaa tgc gat aag gag gaa aag gcc gaa aag gcc aaa att aaa						210
Ala Lys Lys Cys Asp Lys Glu Glu Lys Ala Glu Lys Ala Lys Ile Lys						
	25			30	35	
aag gcc att cag aag ggc aac atg gaa gtt gcg agg ata cac gcc gaa						258
Lys Ala Ile Gln Lys Gly Asn Met Glu Val Ala Arg Ile His Ala Glu						
	40			45	50	
aat gcc atc cgc cag aag aac cag gcg gtg aat ttc ttg aga atg agt						306
Asn Ala Ile Arg Gln Lys Asn Gln Ala Val Asn Phe Leu Arg Met Ser						
	55			60	65	
gcg cga gtc gat gca gtg gct gcc agg gtc cag acg gcg gtg acg atg						354
Ala Arg Val Asp Ala Val Ala Ala Arg Val Gln Thr Ala Val Thr Met						
	70			75	80	85
ggc aag gtg acc aag tcg atg gct ggt gtg gtt aag tcg atg gat gcg						402
Gly Lys Val Thr Lys Ser Met Ala Gly Val Val Lys Ser Met Asp Ala						
	90			95	100	
aca ttg aag acc atg aat ctg gag aag att tct gct ttg atg gac aaa						450
Thr Leu Lys Thr Met Asn Leu Glu Lys Ile Ser Ala Leu Met Asp Lys						
	105			110	115	
ttc gag cac cag ttt gag act ctg gac gtc cag acg cag caa atg gaa						498
Phe Glu His Gln Phe Glu Thr Leu Asp Val Gln Thr Gln Gln Met Glu						
	120			125	130	
gac acg atg agc agc acg acg acg ctc acc act ccc cag aac caa gtg						546
Asp Thr Met Ser Ser Thr Thr Thr Leu Thr Thr Pro Gln Asn Gln Val						
	135			140	145	
gat atg ctg ctc cag gaa atg gca gat gag gcg ggc ctc gac ctc aac						594
Asp Met Leu Leu Gln Glu Met Ala Asp Glu Ala Gly Leu Asp Leu Asn						
	150			155	160	165
atg gag ctg ccg cag ggc cag acc ggc tcc gtg ggc acg agc gtg gct						642
Met Glu Leu Pro Gln Gly Gln Thr Gly Ser Val Gly Thr Ser Val Ala						
	170			175	180	
tcg gcg gag cag gat gaa ctg tct cag aga ctg gcc cgc ctt cgg gat						690
Ser Ala Glu Gln Asp Glu Leu Ser Gln Arg Leu Ala Arg Leu Arg Asp						
	185			190	195	
caa gtg tga cggcagaacc cgctctgagg tttcctggcc atagccaccc						739
Gln Val						
tttgaaatgc tctctgtgtg ttagagagat actataccct agaaactctg aacacgccag						799
aatgctgaaa tgcccttcta cctttgggtt tacagccccc tccacataaa ttaagaaatt						859

cagtatttct gcactcttag ctggattcta aagttctgta tagctcgtaa tgatgggtatt 919  
 tttatagcag ccttttaaca gaactagtta atttcgtgta tatgaatctt tctcgaagat 979  
 ctggtcaaaa ctgtattcag tttcctgccc agaatgatca gattgaaggt ggttggtttt 1039  
 tattattatt tagtgtgatt gatagtatct agaatggcag gtggtgcata aaagttaaag 1099  
 agaggggaaa gattacttag tttggttata cagttataaa caccatgcag tgtattcggt 1159  
 ggactgtgct atttctgttt atcctttggg ttttggtttt tgtttttttt ttttgccttc 1219  
 acagtgcagac tgcaaagat tgttctcata acgtatatta ttaataaatg tggtcctata 1279  
 atttatactg g 1290

<210> 132  
 <211> 199  
 <212> PRT  
 <213> Homo sapiens

<400> 132  
 Met Ser Asn Met Glu Lys His Leu Phe Asn Leu Lys Phe Ala Ala Lys  
 1 5 10 15  
 Glu Leu Ser Arg Ser Ala Lys Lys Cys Asp Lys Glu Glu Lys Ala Glu  
 20 25 30  
 Lys Ala Lys Ile Lys Lys Ala Ile Gln Lys Gly Asn Met Glu Val Ala  
 35 40 45  
 Arg Ile His Ala Glu Asn Ala Ile Arg Gln Lys Asn Gln Ala Val Asn  
 50 55 60  
 Phe Leu Arg Met Ser Ala Arg Val Asp Ala Val Ala Ala Arg Val Gln  
 65 70 75 80  
 Thr Ala Val Thr Met Gly Lys Val Thr Lys Ser Met Ala Gly Val Val  
 85 90 95  
 Lys Ser Met Asp Ala Thr Leu Lys Thr Met Asn Leu Glu Lys Ile Ser  
 100 105 110  
 Ala Leu Met Asp Lys Phe Glu His Gln Phe Glu Thr Leu Asp Val Gln  
 115 120 125  
 Thr Gln Gln Met Glu Asp Thr Met Ser Ser Thr Thr Thr Leu Thr Thr  
 130 135 140  
 Pro Gln Asn Gln Val Asp Met Leu Leu Gln Glu Met Ala Asp Glu Ala  
 145 150 155 160  
 Gly Leu Asp Leu Asn Met Glu Leu Pro Gln Gly Gln Thr Gly Ser Val  
 165 170 175  
 Gly Thr Ser Val Ala Ser Ala Glu Gln Asp Glu Leu Ser Gln Arg Leu  
 180 185 190  
 Ala Arg Leu Arg Asp Gln Val  
 195

<210> 133  
 <211> 564  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (24)..(380)

<400> 133

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gcctgccggg agcttggtgc gct atg gcg aca ccc agc ctg cgg ggt cgt ctg 53
          Met Ala Thr Pro Ser Leu Arg Gly Arg Leu
              1              5              10

gcg cgg ttt ggg aac ccg cgg aag cct gtg ctg aag ccc aat aaa cct 101
Ala Arg Phe Gly Asn Pro Arg Lys Pro Val Leu Lys Pro Asn Lys Pro
              15              20              25

ctc att cta gct aac cgc gtc ggg gag cgg cgc cgg gag aag ggc gag 149
Leu Ile Leu Ala Asn Arg Val Gly Glu Arg Arg Arg Glu Lys Gly Glu
              30              35              40

gcg act tgc atc acg gag atg tcg gtg atg atg gct tgc tgg aag cag 197
Ala Thr Cys Ile Thr Glu Met Ser Val Met Met Ala Cys Trp Lys Gln
              45              50              55

aat gaa ttc cgc gac gat gcg tgc aga aaa gag atc cag ggc ttc ctc 245
Asn Glu Phe Arg Asp Asp Ala Cys Arg Lys Glu Ile Gln Gly Phe Leu
              60              65              70

gat tgt gcc gcg agg gct cag gaa gcc cga aag atg aga tca ata cag 293
Asp Cys Ala Ala Arg Ala Gln Glu Ala Arg Lys Met Arg Ser Ile Gln
              75              80              85              90

gaa acc ctg gga gag tct ggg agt tta ctt cca aat aaa ttg aat aag 341
Glu Thr Leu Gly Glu Ser Gly Ser Leu Leu Pro Asn Lys Leu Asn Lys
              95              100              105

ttg tta cag agg ttt cct aac aaa cct tac ctc agc tga aaatggacaa 390
Leu Leu Gln Arg Phe Pro Asn Lys Pro Tyr Leu Ser
              110              115

gtattttcaa tgactgaaat atagcttctg acaactatgc agaggcattt tagagacatt 450

ggcattgccca tgccctcttt ggagggtaga agaggcaaaa cacttttttc acccttttga 510

atcatagtat gggtagaagt tatgatttat cttgaaataa aatcctctga acag 564

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<210> 134  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<400> 134

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Met Ala Thr Pro Ser Leu Arg Gly Arg Leu Ala Arg Phe Gly Asn Pro
  1              5              10              15
Arg Lys Pro Val Leu Lys Pro Asn Lys Pro Leu Ile Leu Ala Asn Arg
      20              25              30
Val Gly Glu Arg Arg Arg Glu Lys Gly Glu Ala Thr Cys Ile Thr Glu
      35              40              45
Met Ser Val Met Met Ala Cys Trp Lys Gln Asn Glu Phe Arg Asp Asp

```



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70              75              80
tcc ctt ttc ata tcc cga ttc tta agt tct gct att gtg gta ttc tgg 763
Ser Leu Phe Ile Ser Arg Phe Leu Ser Ser Ala Ile Val Val Phe Trp
85              90              95

tgg aga aaa aag aac cgc gtg gct gtt ttt gaa ctg cct gga acc taa 811
Trp Arg Lys Lys Asn Arg Val Ala Val Phe Glu Leu Pro Gly Thr
100              105              110

gaccctgaat tcttttcccc cccaagggga aaatctatat ggaaaacatt tattttaaaa 871

tacaggatga agtgaattaa aagatttaaa tgc 904

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<210> 136  
 <211> 114  
 <212> PRT  
 <213> Homo sapiens

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<400> 136
Met Trp Ala Gln Pro Cys Ala Arg Arg Leu Ala Gly Ile Lys Val Gln
1      5      10      15
Ile Glu Ala Ser Pro Pro Leu Gly Pro Leu Ala Leu Arg Val Phe Ala
20      25      30
Ala Ser Glu Pro Thr Cys Pro Gln Gly His Ser Cys Ile Ser Cys Pro
35      40      45
Ala Val Ile Thr Gly Met Gly Arg Leu Ala Trp Gly His Pro Leu Pro
50      55      60
Leu Pro Gly Cys Cys Cys Val Phe Leu Pro Ala Arg Gly His Cys Gln
65      70      75      80
Asp His Ala Ser Leu Phe Ile Ser Arg Phe Leu Ser Ser Ala Ile Val
85      90      95
Val Phe Trp Trp Arg Lys Lys Asn Arg Val Ala Val Phe Glu Leu Pro
100      105      110
Gly Thr

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<210> 137  
 <211> 472  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (90)..(353)

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<400> 137
aatttccgct tccggtagtg agaacccttc cggtgggcta ggtactgagc gcgcgaggct 60

ctacagagtg aaggtttaaa tccaagggtc atg gca aaa cat ctg aag ttc atc 113
Met Ala Lys His Leu Lys Phe Ile
1      5

gcc agg act gtg atg gta cag gaa ggg aac gtg gaa agc gca tac agg 161
Ala Arg Thr Val Met Val Gln Glu Gly Asn Val Glu Ser Ala Tyr Arg

```

```

10              15              20
acc cta aac aga atc ctc act atg gat ggg ctc att gag gac att aag 209
Thr Leu Asn Arg Ile Leu Thr Met Asp Gly Leu Ile Glu Asp Ile Lys
25              30              35              40

cat cgg cgg tat tat gag aag cca tgc cgc cgg cga cag agg gaa agc 257
His Arg Arg Tyr Tyr Glu Lys Pro Cys Arg Arg Arg Gln Arg Glu Ser
45              50              55

tat gaa agg tgc cgg cgg atc tac aac atg gaa atg gct cgc aag atc 305
Tyr Glu Arg Cys Arg Arg Ile Tyr Asn Met Glu Met Ala Arg Lys Ile
60              65              70

aac ttc ttg atg cga aag aat cgg gca gat ccg tgg cag ggc tgc tga 353
Asn Phe Leu Met Arg Lys Asn Arg Ala Asp Pro Trp Gln Gly Cys
75              80              85

ggcctgtggg tgggacaccc agtgcgaaac cctcatccag ttttctctcc atctcttttc 413
tttgtacaat cccatttcct attaccattc tctgcaataa actcaaatca catgtctgc 472

<210> 138
<211> 87
<212> PRT
<213> Homo sapiens

<400> 138
Met Ala Lys His Leu Lys Phe Ile Ala Arg Thr Val Met Val Gln Glu
1          5          10          15
Gly Asn Val Glu Ser Ala Tyr Arg Thr Leu Asn Arg Ile Leu Thr Met
20          25          30
Asp Gly Leu Ile Glu Asp Ile Lys His Arg Arg Tyr Tyr Glu Lys Pro
35          40          45
Cys Arg Arg Arg Gln Arg Glu Ser Tyr Glu Arg Cys Arg Arg Ile Tyr
50          55          60
Asn Met Glu Met Ala Arg Lys Ile Asn Phe Leu Met Arg Lys Asn Arg
65          70          75          80
Ala Asp Pro Trp Gln Gly Cys
85

<210> 139
<211> 180
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (49)..(168)

<400> 139
attatatatg aattccattc aaatcgttcc tttttgttaa caaggggc atg ggg agg 57
Met Gly Arg
1

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ggt ggg ggt ggg ggg gca gag gcg tct gac ccc agg aac ctg cag ggc 105  
 Gly Gly Gly Gly Gly Ala Glu Ala Ser Asp Pro Arg Asn Leu Gln Gly  
           5                          10                          15

ggg gct ggg tcg gtg ccc tct aag gac aat ttt gac ctt gtt caa cct 153  
 Gly Ala Gly Ser Val Pro Ser Lys Asp Asn Phe Asp Leu Val Gln Pro  
           20                          25                          30                          35

ttc cac aaa gaa taa attgtgtttc ac 180  
 Phe His Lys Glu

<210> 140  
 <211> 39  
 <212> PRT  
 <213> Homo sapiens

<400> 140  
 Met Gly Arg Gly Gly Gly Gly Gly Ala Glu Ala Ser Asp Pro Arg Asn  
       1                          5                          10                          15  
 Leu Gln Gly Gly Ala Gly Ser Val Pro Ser Lys Asp Asn Phe Asp Leu  
                           20                          25                          30  
 Val Gln Pro Phe His Lys Glu  
                           35

<210> 141  
 <211> 473  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (35)..(343)

<400> 141  
 gagacgcaga gtcttgagca ggcgggcagg cacc atg ttc ctg act gcg ctc ctc 55  
   Met Phe Leu Thr Ala Leu Leu  
   1  5

tgg cgc ggc cgc att ccc ggc cgt cag tgg atc ggg aag cac cgg cgg 103  
 Trp Arg Gly Arg Ile Pro Gly Arg Gln Trp Ile Gly Lys His Arg Arg  
           10                          15                          20

ccg cgg ttc gtg tcg ttg cgc gcc aag cag aac atg atc cgc cgc ctg 151  
 Pro Arg Phe Val Ser Leu Arg Ala Lys Gln Asn Met Ile Arg Arg Leu  
           25                          30                          35

gag atc gag gcg gag aac cat tac tgg ctg agc atg ccc tac atg acc 199  
 Glu Ile Glu Ala Glu Asn His Tyr Trp Leu Ser Met Pro Tyr Met Thr  
           40                          45                          50                          55

cgg gag cag gag cgc ggc cac gcc gcg gtg cgc agg agg gag gcc ttc 247  
 Arg Glu Gln Glu Arg Gly His Ala Ala Val Arg Arg Arg Glu Ala Phe  
                           60                          65                          70

# COLORED

# COLORED

# C O C O

[illegible]

# C O C O

# COLORED

# COLORED

# COLORED

# C O C O

[illegible]

# C O C O

# C O C O

[illegible]

# C O C O

# COLORED

# COLORED

# C O C K

# COLORED

[illegible][illegible]

# COLORED

# COLORED

# COLORED

# COLORED

# COLORED

# C O C O

# COLORED

[illegible]

agc gtc atc cag aac ctg ccc aag aac ggt tct tac cgc ccc tcc tat	213
Ser Val Ile Gln Asn Leu Pro Lys Asn Gly Ser Tyr Arg Pro Ser Tyr	
25 30 35	
gaa gag atg ctg cga ttc tac agt tac tac aag cag gcc acc atg ggg	261
Glu Glu Met Leu Arg Phe Tyr Ser Tyr Tyr Lys Gln Ala Thr Met Gly	
40 45 50	
ccc tgc ctg gtc ccc cgg ccc ggg ttc tgg gac ccc att gga cga tat	309
Pro Cys Leu Val Pro Arg Pro Gly Phe Trp Asp Pro Ile Gly Arg Tyr	
55 60 65	
aag tgg gac gcc tgg aac agt ctg ggc aag atg agc agg gag gag gcc	357
Lys Trp Asp Ala Trp Asn Ser Leu Gly Lys Met Ser Arg Glu Glu Ala	
70 75 80	
atg tct gcc tac atc act gaa atg aaa ctg gtg gca cag aag gtg atc	405
Met Ser Ala Tyr Ile Thr Glu Met Lys Leu Val Ala Gln Lys Val Ile	
85 90 95 100	
gac aca gtg ccc ctg ggt gag gtg gca gag gac atg ttt ggt tac ttc	453
Asp Thr Val Pro Leu Gly Glu Val Ala Glu Asp Met Phe Gly Tyr Phe	
105 110 115	
gag ccc ctg tac cag gtg atc cct gac atg ccg agg ccc cca gag acc	501
Glu Pro Leu Tyr Gln Val Ile Pro Asp Met Pro Arg Pro Pro Glu Thr	
120 125 130	
ttc ctg aga agg gtc aca ggt tgg aaa gag cag gtt gtg aat gga gat	549
Phe Leu Arg Arg Val Thr Gly Trp Lys Glu Gln Val Val Asn Gly Asp	
135 140 145	
gtt ggg gct gtt tca gag cct ccc tgc ctc ccc aag gaa ccg gca ccc	597
Val Gly Ala Val Ser Glu Pro Pro Cys Leu Pro Lys Glu Pro Ala Pro	
150 155 160	
cca agc cca gct tcc ctc tgg gca gta act cta cca acc cct cca cag	645
Pro Ser Pro Ala Ser Leu Trp Ala Val Thr Leu Pro Thr Pro Pro Gln	
165 170 175 180	
agt ccc att cac cca ggg acc tgg act ccg agg ttt tct gtg att ccc	693
Ser Pro Ile His Pro Gly Thr Trp Thr Pro Arg Phe Ser Val Ile Pro	
185 190 195	
tgg agc agc tgg agc ctg agc tgg ttt gga cag agc agc ggg cag cat	741
Trp Ser Ser Trp Ser Leu Ser Trp Phe Gly Gln Ser Ser Gly Gln His	
200 205 210	
ctg gag gaa agc gtg atc cca gga aca gcc ccg tgc ccc cca caa aga	789
Leu Glu Glu Ser Val Ile Pro Gly Thr Ala Pro Cys Pro Pro Gln Arg	
215 220 225	
aag agg ggt tgc ggg gca gcc cgc cgg ggc ccc agg agt tgg acg tgt	837
Lys Arg Gly Cys Gly Ala Ala Arg Arg Gly Pro Arg Ser Trp Thr Cys	
230 235 240	
ggc tgc tgg gga cag ttc gag cac tac agg aga gca tgc agg agg tgc	885

Gly Cys Trp Gly Gln Phe Glu His Tyr Arg Arg Ala Cys Arg Arg Cys  
 245 250 255 260

agg cga ggg tgc aga gcc tgg aga gca tgc ccc ggc ccc ctg agc aga 933  
 Arg Arg Gly Cys Arg Ala Trp Arg Ala Cys Pro Gly Pro Leu Ser Arg  
 265 270 275

ggc cgc agc cca ggc cca gtg ctc ggc cat ggc ccc ttg ggc tcc cgg 981  
 Gly Arg Ser Pro Gly Pro Val Leu Gly His Gly Pro Leu Gly Ser Arg  
 280 285 290

ggc ccg cgc tgc tct tct tcc tcc tgt ggc cct tcg tcg tcc agt ggc 1029  
 Gly Pro Arg Cys Ser Ser Ser Ser Cys Gly Pro Ser Ser Ser Ser Gly  
 295 300 305

tct tcc gaa tgt ttc gga ccc aaa aga ggt gac tgt cag tgg agg ggt 1077  
 Ser Ser Glu Cys Phe Gly Pro Lys Arg Gly Asp Cys Gln Trp Arg Gly  
 310 315 320

ctc tgc agc caa ctg aga cta tct tgc tgt gcc ctg agc ctt cct agg 1125  
 Leu Cys Ser Gln Leu Arg Leu Ser Cys Cys Ala Leu Ser Leu Pro Arg  
 325 330 335 340

gtt tag aagaacagca ttcaaaattc ccggtcctgt cagtgtttgc cttcgcacct 1181  
 Val

cctcccctaa agcagcgcg ggggcaaata agacccacc cctccctgca gcttcacagg 1241

gacgcttcct tccctccccg caaccacccc aggctcccct gggaggctgc agttgtggta 1301

cacgtccccg gtgctggggt ggccgtgact cgggggcggg gcgatcggggt ctcagcccct 1361

gccttcccca gtctctgggt caccgaatt tccccacccc tgcttctccc cgaggagggt 1421

gagctcttga gcaagttggg acttgggccc gggcctggaa gaatgattgg ctgggaggcc 1481

gcgggaggga ggccaggagg cccggaccag ttgggaggag tgagcaggcc ccgggggagg 1541

gggatgagcg cagtttgctc gctttcctcc cctgccggcc ccctccgccc ccacacacac 1601

tcgggacgtc ttcattgaag attcacttac aaaggaatgt ttcactaaat aaaagaaaac 1661

cag 1664

<210> 144  
 <211> 341  
 <212> PRT  
 <213> Homo sapiens

<400> 144  
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 1 5 10 15  
 Gln Ala Ala Val Ser Val Ile Gln Asn Leu Pro Lys Asn Gly Ser Tyr  
 20 25 30  
 Arg Pro Ser Tyr Glu Glu Met Leu Arg Phe Tyr Ser Tyr Tyr Lys Gln  
 35 40 45

09890688-092701

Ala	Thr	Met	Gly	Pro	Cys	Leu	Val	Pro	Arg	Pro	Gly	Phe	Trp	Asp	Pro
50						55					60				
Ile	Gly	Arg	Tyr	Lys	Trp	Asp	Ala	Trp	Asn	Ser	Leu	Gly	Lys	Met	Ser
65					70				75						80
Arg	Glu	Glu	Ala	Met	Ser	Ala	Tyr	Ile	Thr	Glu	Met	Lys	Leu	Val	Ala
				85					90					95	
Gln	Lys	Val	Ile	Asp	Thr	Val	Pro	Leu	Gly	Glu	Val	Ala	Glu	Asp	Met
			100					105					110		
Phe	Gly	Tyr	Phe	Glu	Pro	Leu	Tyr	Gln	Val	Ile	Pro	Asp	Met	Pro	Arg
		115					120					125			
Pro	Pro	Glu	Thr	Phe	Leu	Arg	Arg	Val	Thr	Gly	Trp	Lys	Glu	Gln	Val
	130					135					140				
Val	Asn	Gly	Asp	Val	Gly	Ala	Val	Ser	Glu	Pro	Pro	Cys	Leu	Pro	Lys
145					150					155					160
Glu	Pro	Ala	Pro	Pro	Ser	Pro	Ala	Ser	Leu	Trp	Ala	Val	Thr	Leu	Pro
				165					170					175	
Thr	Pro	Pro	Gln	Ser	Pro	Ile	His	Pro	Gly	Thr	Trp	Thr	Pro	Arg	Phe
			180					185					190		
Ser	Val	Ile	Pro	Trp	Ser	Ser	Trp	Ser	Leu	Ser	Trp	Phe	Gly	Gln	Ser
		195					200					205			
Ser	Gly	Gln	His	Leu	Glu	Glu	Ser	Val	Ile	Pro	Gly	Thr	Ala	Pro	Cys
	210					215					220				
Pro	Pro	Gln	Arg	Lys	Arg	Gly	Cys	Gly	Ala	Ala	Arg	Arg	Gly	Pro	Arg
225					230					235					240
Ser	Trp	Thr	Cys	Gly	Cys	Trp	Gly	Gln	Phe	Glu	His	Tyr	Arg	Arg	Ala
				245					250					255	
Cys	Arg	Arg	Cys	Arg	Arg	Gly	Cys	Arg	Ala	Trp	Arg	Ala	Cys	Pro	Gly
			260					265					270		
Pro	Leu	Ser	Arg	Gly	Arg	Ser	Pro	Gly	Pro	Val	Leu	Gly	His	Gly	Pro
		275					280					285			
Leu	Gly	Ser	Arg	Gly	Pro	Arg	Cys	Ser	Ser	Ser	Ser	Cys	Gly	Pro	Ser
	290					295						300			
Ser	Ser	Ser	Gly	Ser	Ser	Glu	Cys	Phe	Gly	Pro	Lys	Arg	Gly	Asp	Cys
305					310				315						320
Gln	Trp	Arg	Gly	Leu	Cys	Ser	Gln	Leu	Arg	Leu	Ser	Cys	Cys	Ala	Leu
				325					330					335	
Ser	Leu	Pro	Arg	Val											
			340												

<210> 145  
 <211> 835  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (90)..(740)

<400> 145  
 aaaaatccga agtgccgcgg aaagtggaga gctgacaagg aaggtttcga gcgttttgct 60  
 ggcaaaggga tttcttataaa cctccaggc atg cgt ctt tct gcc ctg ctg gcc 113  
 Met Arg Leu Ser Ala Leu Leu Ala  
 1 5  
 ttg gca tcc aag gtc act ctg ccc ccc cat tac cgc tat ggg atg agc 161

Leu	Ala	Ser	Lys	Val	Thr	Leu	Pro	Pro	His	Tyr	Arg	Tyr	Gly	Met	Ser		
10						15					20						
ccc	cca	ggc	tct	gtt	gca	gac	aag	agg	aag	aac	ccc	cca	tgg	atc	agg	209	
Pro	Pro	Gly	Ser	Val	Ala	Asp	Lys	Arg	Lys	Asn	Pro	Pro	Trp	Ile	Arg		
25					30					35					40		
cgg	cgc	cca	gtg	gtt	gtg	gaa	ccc	atc	tct	gat	gaa	gac	tgg	tat	ctg	257	
Arg	Arg	Pro	Val	Val	Val	Glu	Pro	Ile	Ser	Asp	Glu	Asp	Trp	Tyr	Leu		
				45				50						55			
ttc	tgt	ggg	gac	acg	gtg	gag	atc	cta	gaa	ggc	aag	gat	gcc	ggg	aag	305	
Phe	Cys	Gly	Asp	Thr	Val	Glu	Ile	Leu	Glu	Gly	Lys	Asp	Ala	Gly	Lys		
			60					65					70				
cag	ggc	aaa	gtg	gtt	caa	gtt	atc	cgg	cag	cga	aac	tgg	gtg	gtc	gtg	353	
Gln	Gly	Lys	Val	Val	Gln	Val	Ile	Arg	Gln	Arg	Asn	Trp	Val	Val	Val		
		75					80					85					
gga	ggg	ctg	aac	aca	cat	tac	cgc	tac	att	ggc	aag	acc	atg	gat	tac	401	
Gly	Gly	Leu	Asn	Thr	His	Tyr	Arg	Tyr	Ile	Gly	Lys	Thr	Met	Asp	Tyr		
	90					95					100						
cgg	gga	acc	atg	atc	cct	agt	gaa	gcc	ccc	ttg	ctc	cac	cgc	cag	gtc	449	
Arg	Gly	Thr	Met	Ile	Pro	Ser	Glu	Ala	Pro	Leu	Leu	His	Arg	Gln	Val		
105					110					115					120		
aaa	ctt	gtg	gat	cct	atg	gac	agg	aaa	ccc	act	gag	atc	gag	tgg	aga	497	
Lys	Leu	Val	Asp	Pro	Met	Asp	Arg	Lys	Pro	Thr	Glu	Ile	Glu	Trp	Arg		
				125					130					135			
ttt	act	gaa	gca	gga	gag	cgg	gta	cga	gtc	tcc	aca	cga	tca	ggg	aga	545	
Phe	Thr	Glu	Ala	Gly	Glu	Arg	Val	Arg	Val	Ser	Thr	Arg	Ser	Gly	Arg		
			140					145					150				
att	atc	cct	aaa	ccc	gaa	ttt	ccc	aga	gct	gat	ggc	atc	gtc	cct	gaa	593	
Ile	Ile	Pro	Lys	Pro	Glu	Phe	Pro	Arg	Ala	Asp	Gly	Ile	Val	Pro	Glu		
		155					160					165					
acg	tgg	att	gat	ggc	ccc	aaa	gac	aca	tca	gtg	gaa	gat	gct	tta	gaa	641	
Thr	Trp	Ile	Asp	Gly	Pro	Lys	Asp	Thr	Ser	Val	Glu	Asp	Ala	Leu	Glu		
	170					175					180						
aga	acc	tat	gtg	ccc	tgt	cta	aag	aca	ctg	cag	gag	gag	gtg	atg	gag	689	
Arg	Thr	Tyr	Val	Pro	Cys	Leu	Lys	Thr	Leu	Gln	Glu	Glu	Val	Met	Glu		
185					190					195					200		
gcc	atg	ggg	atc	aag	gag	acc	cgg	aaa	tac	aag	aag	gtc	tat	tgg	tat	737	
Ala	Met	Gly	Ile	Lys	Glu	Thr	Arg	Lys	Tyr	Lys	Lys	Val	Tyr	Trp	Tyr		
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 <212> PRT  
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<400> 146  
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 Ile Ser Asp Glu Asp Trp Tyr Leu Phe Cys Gly Asp Thr Val Glu Ile  
 50 55 60  
 Leu Glu Gly Lys Asp Ala Gly Lys Gln Gly Lys Val Val Gln Val Ile  
 65 70 75 80  
 Arg Gln Arg Asn Trp Val Val Val Gly Gly Leu Asn Thr His Tyr Arg  
 85 90 95  
 Tyr Ile Gly Lys Thr Met Asp Tyr Arg Gly Thr Met Ile Pro Ser Glu  
 100 105 110  
 Ala Pro Leu Leu His Arg Gln Val Lys Leu Val Asp Pro Met Asp Arg  
 115 120 125  
 Lys Pro Thr Glu Ile Glu Trp Arg Phe Thr Glu Ala Gly Glu Arg Val  
 130 135 140  
 Arg Val Ser Thr Arg Ser Gly Arg Ile Ile Pro Lys Pro Glu Phe Pro  
 145 150 155 160  
 Arg Ala Asp Gly Ile Val Pro Glu Thr Trp Ile Asp Gly Pro Lys Asp  
 165 170 175  
 Thr Ser Val Glu Asp Ala Leu Glu Arg Thr Tyr Val Pro Cys Leu Lys  
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 Lys Tyr Lys Lys Val Tyr Trp Tyr  
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 Met Lys Ala Val Lys Ser Glu Arg Glu Arg Gly Ser Arg  
 1 5 10  
 cga aga cac cgg gac ggg gac gtg gtg ctg ccg gcg ggg gtg gtg gtg 157  
 Arg Arg His Arg Asp Gly Asp Val Val Leu Pro Ala Gly Val Val Val  
 15 20 25  
 aag cag gag cgt ctc agc cca gaa gtc gca cct ccc gcc cac cgc cgt 205

Lys	Gln	Glu	Arg	Leu	Ser	Pro	Glu	Val	Ala	Pro	Pro	Ala	His	Arg	Arg	
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ccg	gac	cac	tcc	ggt	ggt	agc	ccg	tct	ccg	ccg	acc	agc	gag	ccg	gcc	253
Pro	Asp	His	Ser	Gly	Gly	Ser	Pro	Ser	Pro	Pro	Thr	Ser	Glu	Pro	Ala	
				50					55					60		
cgc	tcg	ggc	cac	cgc	ggg	aac	cga	gcc	cga	gga	gtt	agc	cgg	tcc	cca	301
Arg	Ser	Gly	His	Arg	Gly	Asn	Arg	Ala	Arg	Gly	Val	Ser	Arg	Ser	Pro	
			65					70					75			
ccc	aaa	aag	aaa	aac	aag	gcc	tca	ggg	aga	aga	agc	aag	tct	cct	cgc	349
Pro	Lys	Lys	Lys	Asn	Lys	Ala	Ser	Gly	Arg	Arg	Ser	Lys	Ser	Pro	Arg	
		80					85					90				
agt	aag	aga	aac	cga	agt	cct	cac	cac	tca	aca	gtc	aaa	gtg	aag	cag	397
Ser	Lys	Arg	Asn	Arg	Ser	Pro	His	His	Ser	Thr	Val	Lys	Val	Lys	Gln	
	95					100					105					
gag	cgt	gag	gat	cat	ccc	cgg	aga	gga	cgg	gag	gat	cgg	cag	cac	agg	445
Glu	Arg	Glu	Asp	His	Pro	Arg	Arg	Gly	Arg	Glu	Asp	Arg	Gln	His	Arg	
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gaa	cca	tca	gaa	cag	gaa	cac	agg	aga	gct	agg	aac	agt	gac	cgg	gac	493
Glu	Pro	Ser	Glu	Gln	Glu	His	Arg	Arg	Ala	Arg	Asn	Ser	Asp	Arg	Asp	
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aga	cac	cgg	ggc	cat	tcc	cac	caa	agg	aga	acg	tct	aac	gag	agg	cct	541
Arg	His	Arg	Gly	His	Ser	His	Gln	Arg	Arg	Thr	Ser	Asn	Glu	Arg	Pro	
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ggg	agt	ggg	cag	ggt	cag	gga	cgg	gat	cga	gac	act	cag	aac	ctg	cag	589
Gly	Ser	Gly	Gln	Gly	Gln	Gly	Arg	Asp	Arg	Asp	Thr	Gln	Asn	Leu	Gln	
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gct	cag	gaa	gaa	gag	cgg	gag	ttt	tat	aat	gcc	agg	cga	cgg	gag	cat	637
Ala	Gln	Glu	Glu	Glu	Arg	Glu	Phe	Tyr	Asn	Ala	Arg	Arg	Arg	Glu	His	
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cgc	cag	agg	aat	gac	gtt	ggt	ggc	ggc	agt	gag	tct	cag	gag	ttg		685
Arg	Gln	Arg	Asn	Asp	Val	Gly	Gly	Gly	Ser	Glu	Ser	Gln	Glu	Leu		
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gtt	cct	cgg	cct	ggt	ggc	aac	aac	aaa	gaa	aaa	gag	gtg	ccc	gct	aaa	733
Val	Pro	Arg	Pro	Gly	Gly	Asn	Asn	Lys	Glu	Lys	Glu	Val	Pro	Ala	Lys	
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gaa	aaa	cca	agc	ttt	gaa	ctt	tct	ggg	gca	ctt	ctt	gag	gac	acc	aac	781
Glu	Lys	Pro	Ser	Phe	Glu	Leu	Ser	Gly	Ala	Leu	Leu	Glu	Asp	Thr	Asn	
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act	ttc	cgg	ggt	gta	gtc	att	aaa	tat	agt	gag	ccc	cca	gaa	gca	cgt	829
Thr	Phe	Arg	Gly	Val	Val	Ile	Lys	Tyr	Ser	Glu	Pro	Pro	Glu	Ala	Arg	
	240					245					250					
atc	ccc	aaa	aaa	cgg	tgg	cgt	ctc	tac	cca	ttt	aaa	aat	gat	gag	gtg	877
Ile	Pro	Lys	Lys	Arg	Trp	Arg	Leu	Tyr	Pro	Phe	Lys	Asn	Asp	Glu	Val	

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Leu Pro Val Met Tyr Ile His Arg Gln Ser Ala Tyr Leu Leu Gly Arg			
270	275	280	285
cac cgc cgc att gca gac att cca att gat cac ccg tct tgt tca aag			973
His Arg Arg Ile Ala Asp Ile Pro Ile Asp His Pro Ser Cys Ser Lys			
290	295		300
cag cat gcg gtc ttt caa tat cgg ctt gtg gaa tat acc cgt gct gat			1021
Gln His Ala Val Phe Gln Tyr Arg Leu Val Glu Tyr Thr Arg Ala Asp			
305	310		315
ggc aca gtt ggc cga aga gtg aag ccc tac atc att gac ctt ggc tca			1069
Gly Thr Val Gly Arg Arg Val Lys Pro Tyr Ile Ile Asp Leu Gly Ser			
320	325		330
ggc aat gga acc ttc tta aac aac aaa cgt att gag cca cag aga tac			1117
Gly Asn Gly Thr Phe Leu Asn Asn Lys Arg Ile Glu Pro Gln Arg Tyr			
335	340		345
tat gaa cta aaa gaa aag gat gta ctc aaa ttt gga ttc agt agc aga			1165
Tyr Glu Leu Lys Glu Lys Asp Val Leu Lys Phe Gly Phe Ser Ser Arg			
350	355		360
gaa tac gtc ttg ctc cat gag tcg tcg gac act tct gaa ata gac agg			1213
Glu Tyr Val Leu Leu His Glu Ser Ser Asp Thr Ser Glu Ile Asp Arg			
370	375		380
aaa gat gac gag gat gag gag gag gag gaa gaa gtg tct gac agc tag			1261
Lys Asp Asp Glu Asp Glu Glu Glu Glu Glu Glu Val Ser Asp Ser			
385	390		395
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 atat 2465

<210> 148  
 <211> 396  
 <212> PRT  
 <213> Homo sapiens

<400> 148

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Arg	Leu	Ser	Pro	Glu	Val	Ala	Pro	Pro	Ala	His	Arg	Arg	Pro	Asp	His
		35					40					45			
Ser	Gly	Gly	Ser	Pro	Ser	Pro	Pro	Thr	Ser	Glu	Pro	Ala	Arg	Ser	Gly
	50					55					60				
His	Arg	Gly	Asn	Arg	Ala	Arg	Gly	Val	Ser	Arg	Ser	Pro	Pro	Lys	Lys
	65				70					75				80	
Lys	Asn	Lys	Ala	Ser	Gly	Arg	Arg	Ser	Lys	Ser	Pro	Arg	Ser	Lys	Arg
				85					90					95	
Asn	Arg	Ser	Pro	His	His	Ser	Thr	Val	Lys	Val	Lys	Gln	Glu	Arg	Glu
			100					105					110		
Asp	His	Pro	Arg	Arg	Gly	Arg	Glu	Asp	Arg	Gln	His	Arg	Glu	Pro	Ser
	115						120					125			
Glu	Gln	Glu	His	Arg	Arg	Ala	Arg	Asn	Ser	Asp	Arg	Asp	Arg	His	Arg
	130					135					140				
Gly	His	Ser	His	Gln	Arg	Arg	Thr	Ser	Asn	Glu	Arg	Pro	Gly	Ser	Gly
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Gln	Gly	Gln	Gly	Arg	Asp	Arg	Asp	Thr	Gln	Asn	Leu	Gln	Ala	Gln	Glu
				165				170						175	
Glu	Glu	Arg	Glu	Phe	Tyr	Asn	Ala	Arg	Arg	Arg	Glu	His	Arg	Gln	Arg
			180				185					190			
Asn	Asp	Val	Gly	Gly	Gly	Gly	Ser	Glu	Ser	Gln	Glu	Leu	Val	Pro	Arg
	195						200					205			
Pro	Gly	Gly	Asn	Asn	Lys	Glu	Lys	Glu	Val	Pro	Ala	Lys	Glu	Lys	Pro
	210					215					220				
Ser	Phe	Glu	Leu	Ser	Gly	Ala	Leu	Leu	Glu	Asp	Thr	Asn	Thr	Phe	Arg
225					230					235				240	
Gly	Val	Val	Ile	Lys	Tyr	Ser	Glu	Pro	Pro	Glu	Ala	Arg	Ile	Pro	Lys



75	80	85	
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cag gag ctg aag gac ccc aat gag gat gag cca aac atc cga gtg ctc Gln Glu Leu Lys Asp Pro Asn Glu Asp Glu Pro Asn Ile Arg Val Leu 125 130 135			556
ctt gag cac cgc ttt tac aag gag aag agc aag agc gtc aag cag acc Leu Glu His Arg Phe Tyr Lys Glu Lys Ser Lys Ser Val Lys Gln Thr 140 145 150			604
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acc tgc aca ggg tgt tat tac cgc tgt cac agt aag tgc ttg aac ctc Thr Cys Thr Gly Cys Tyr Tyr Arg Cys His Ser Lys Cys Leu Asn Leu 170 175 180			700
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gaa ctg aac atc tgc cct gag aca ggg ctg gac agc cag gat tac cgc Glu Leu Asn Ile Cys Pro Glu Thr Gly Leu Asp Ser Gln Asp Tyr Arg 205 210 215			796
tgt gcc gag tgc cgg gcg ccc atc tct ctg cgg ggt gtg ccc agt gag Cys Ala Glu Cys Arg Ala Pro Ile Ser Leu Arg Gly Val Pro Ser Glu 220 225 230			844
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Ile Leu Leu Met Lys Pro Tyr Phe Ile Thr Cys Arg Glu Ala Met Glu	
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gac gag atg tac tct gtc cag gac ctc ctg gac gtg cat gcc ggc cgc	1228
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Leu Gly Cys Ser Leu Thr Glu Ile His Thr Leu Phe Ala Lys His Ile	
365 370 375	
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Lys Leu Asp Cys Glu Arg Cys Gln Ala Lys Gly Phe Val Cys Glu Leu	
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Cys Arg Glu Gly Asp Val Leu Phe Pro Phe Asp Ser His Thr Ser Val	
395 400 405	
tgc gcc gac tgc tcc gcg gtc ttc cac agg gac tgc tac tac gac aac	1420
Cys Ala Asp Cys Ser Ala Val Phe His Arg Asp Cys Tyr Tyr Asp Asn	
410 415 420	
tcc acc act tgt ccc aag tgt gcc cgg ctc agc ctg agg aag cag tgc	1468
Ser Thr Thr Cys Pro Lys Cys Ala Arg Leu Ser Leu Arg Lys Gln Ser	
425 430 435 440	
ctc ttc cag gag cca ggt ccc gat gtg gag gcc tag cgccgaggaa	1514
Leu Phe Gln Glu Pro Gly Pro Asp Val Glu Ala	
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<212> PRT  
<213> Homo sapiens

<400> 150

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		20						25					30		
Glu	Glu	Val	Pro	Asp	Val	Thr	Pro	Glu	Glu	Ala	Leu	Pro	Glu	Leu	Pro
		35					40					45			
Pro	Gly	Glu	Pro	Glu	Phe	Arg	Cys	Pro	Glu	Arg	Val	Met	Asp	Leu	Gly
	50					55					60				
Leu	Ser	Glu	Asp	His	Phe	Ser	Arg	Pro	Val	Gly	Leu	Phe	Leu	Ala	Ser
	65				70					75					80
Asp	Val	Gln	Gln	Leu	Arg	Gln	Ala	Ile	Glu	Glu	Cys	Lys	Gln	Val	Ile
				85					90					95	
Leu	Glu	Leu	Pro	Glu	Gln	Ser	Glu	Lys	Gln	Lys	Asp	Ala	Val	Val	Arg
			100					105					110		
Leu	Ile	His	Leu	Arg	Leu	Lys	Leu	Gln	Glu	Leu	Lys	Asp	Pro	Asn	Glu
	115						120					125			
Asp	Glu	Pro	Asn	Ile	Arg	Val	Leu	Leu	Glu	His	Arg	Phe	Tyr	Lys	Glu
	130					135					140				
Lys	Ser	Lys	Ser	Val	Lys	Gln	Thr	Cys	Asp	Lys	Cys	Asn	Thr	Ile	Ile
	145				150					155					160
Trp	Gly	Leu	Ile	Gln	Thr	Trp	Tyr	Thr	Cys	Thr	Gly	Cys	Tyr	Tyr	Arg
			165						170					175	
Cys	His	Ser	Lys	Cys	Leu	Asn	Leu	Ile	Ser	Lys	Pro	Cys	Val	Ser	Ser
			180					185					190		
Lys	Val	Ser	His	Gln	Ala	Glu	Tyr	Glu	Leu	Asn	Ile	Cys	Pro	Glu	Thr
	195						200					205			
Gly	Leu	Asp	Ser	Gln	Asp	Tyr	Arg	Cys	Ala	Glu	Cys	Arg	Ala	Pro	Ile
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Ser	Leu	Arg	Gly	Val	Pro	Ser	Glu	Ala	Arg	Gln	Cys	Asp	Tyr	Thr	Gly
	225				230					235					240
Gln	Tyr	Tyr	Cys	Ser	His	Cys	His	Trp	Asn	Asp	Leu	Ala	Val	Ile	Pro
				245					250					255	
Ala	Arg	Val	Val	His	Asn	Trp	Asp	Phe	Glu	Pro	Arg	Lys	Val	Ser	Arg
			260					265					270		
Cys	Ser	Met	Arg	Tyr	Leu	Ala	Leu	Met	Val	Ser	Arg	Pro	Val	Leu	Arg
		275					280					285			
Leu	Arg	Glu	Ile	Asn	Pro	Leu	Leu	Phe	Ser	Tyr	Val	Glu	Glu	Leu	Val
	290					295					300				
Glu	Ile	Arg	Lys	Leu	Arg	Gln	Asp	Ile	Leu	Leu	Met	Lys	Pro	Tyr	Phe
	305				310					315					320
Ile	Thr	Cys	Arg	Glu	Ala	Met	Glu	Ala	Arg	Leu	Leu	Leu	Gln	Leu	Gln
				325					330					335	
Asp	Arg	Gln	His	Phe	Val	Glu	Asn	Asp	Glu	Met	Tyr	Ser	Val	Gln	Asp
			340					345					350		
Leu	Leu	Asp	Val	His	Ala	Gly	Arg	Leu	Gly	Cys	Ser	Leu	Thr	Glu	Ile
		355					360					365			
His	Thr	Leu	Phe	Ala	Lys	His	Ile	Lys	Leu	Asp	Cys	Glu	Arg	Cys	Gln
	370					375					380				
Ala	Lys	Gly	Phe	Val	Cys	Glu	Leu	Cys	Arg	Glu	Gly	Asp	Val	Leu	Phe
	385				390					395					400
Pro	Phe	Asp	Ser	His	Thr	Ser	Val	Cys	Ala	Asp	Cys	Ser	Ala	Val	Phe
				405					410					415	
His	Arg	Asp	Cys	Tyr	Tyr	Asp	Asn	Ser	Thr	Thr	Cys	Pro	Lys	Cys	Ala
			420				425					430			
Arg	Leu	Ser	Leu	Arg	Lys	Gln	Ser	Leu	Phe	Gln	Glu	Pro	Gly	Pro	Asp
		435					440					445			
Val	Glu	Ala													

450

<210> 151  
 <211> 442  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (12)..(353)

<400> 151  
 gttctacagc t atg gcc ggg cca gct gca gct ttc cgc cgc ttg ggc gcc 50  
           Met Ala Gly Pro Ala Ala Ala Phe Arg Arg Leu Gly Ala  
               1                  5                  10  
  
 ttg tcc gga gct gcg gcc tta ggc ttc gct tcc tac ggg gcg cac ggc 98  
 Leu Ser Gly Ala Ala Ala Leu Gly Phe Ala Ser Tyr Gly Ala His Gly  
       15                  20                  25  
  
 gcc caa ttc cca gat gcc tac ggg aag gag ctg ttt gac aag gcc aac 146  
 Ala Gln Phe Pro Asp Ala Tyr Gly Lys Glu Leu Phe Asp Lys Ala Asn  
       30                  35                  40                  45  
  
 aaa cac cac ttc tta cac agc ctg gcc ctg tta ggg gtg ccc cat tgc 194  
 Lys His His Phe Leu His Ser Leu Ala Leu Leu Gly Val Pro His Cys  
           50                  55                  60  
  
 aga aag cca ctc tgg gct ggg tta ttg cta gct tcc gga acg acc tta 242  
 Arg Lys Pro Leu Trp Ala Gly Leu Leu Leu Ala Ser Gly Thr Thr Leu  
       65                  70                  75  
  
 ttc tgc acc agc ttt tac tac cag gct ctg agt gga gac ccc agc atc 290  
 Phe Cys Thr Ser Phe Tyr Tyr Gln Ala Leu Ser Gly Asp Pro Ser Ile  
       80                  85                  90  
  
 cag act ttg gcc cct gcg gga ggg acc ctg cta ctc ttg ggc tgg ctt 338  
 Gln Thr Leu Ala Pro Ala Gly Gly Thr Leu Leu Leu Leu Gly Trp Leu  
       95                  100                  105  
  
 gcc ttg gct ctt tga gctccctttt gcttaattac tgggttttct gggcagtttt 393  
 Ala Leu Ala Leu  
 110  
  
 ttttttttaa gagttggagt aagaagagga ttaaaaagga aaggcaaat 442

<210> 152  
 <211> 113  
 <212> PRT  
 <213> Homo sapiens

<400> 152  
 Met Ala Gly Pro Ala Ala Ala Phe Arg Arg Leu Gly Ala Leu Ser Gly  
       1                  5                  10                  15  
 Ala Ala Ala Leu Gly Phe Ala Ser Tyr Gly Ala His Gly Ala Gln Phe

		20						25					30				
Pro	Asp	Ala	Tyr	Gly	Lys	Glu	Leu	Phe	Asp	Lys	Ala	Asn	Lys	His	His		
		35					40					45					
Phe	Leu	His	Ser	Leu	Ala	Leu	Leu	Gly	Val	Pro	His	Cys	Arg	Lys	Pro		
	50					55					60						
Leu	Trp	Ala	Gly	Leu	Leu	Leu	Ala	Ser	Gly	Thr	Thr	Leu	Phe	Cys	Thr		
	65				70					75					80		
Ser	Phe	Tyr	Tyr	Gln	Ala	Leu	Ser	Gly	Asp	Pro	Ser	Ile	Gln	Thr	Leu		
				85					90					95			
Ala	Pro	Ala	Gly	Gly	Thr	Leu	Leu	Leu	Leu	Gly	Trp	Leu	Ala	Leu	Ala		
			100					105					110				
Leu																	

<210> 153  
 <211> 726  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (12)..(680)

<400> 153  
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 Met Ala Ala Ser Val Arg Gln Ala Arg Ser Leu Leu Gly  
 1 5 10

gtg gcg gcg acc ctg gcc ccg ggt tcc cgt ggc tac cgg gcg ccg ccg 98  
 Val Ala Ala Thr Leu Ala Pro Gly Ser Arg Gly Tyr Arg Ala Arg Pro  
 15 20 25

ccc ccg cgc cgc agg ccg gga ccc cgg tgg cca gac ccc gag gac ctc 146  
 Pro Pro Arg Arg Arg Pro Gly Pro Arg Trp Pro Asp Pro Glu Asp Leu  
 30 35 40 45

ctg acc ccg cgg tgg cag ctg gga ccg cgc tac gcg gct aag cag ttc 194  
 Leu Thr Pro Arg Trp Gln Leu Gly Pro Arg Tyr Ala Ala Lys Gln Phe  
 50 55 60

gcg cgt tac ggc gcc gcc tcc ggg gtg gtc ccc ggt tcg tta tgg ccg 242  
 Ala Arg Tyr Gly Ala Ala Ser Gly Val Val Pro Gly Ser Leu Trp Pro  
 65 70 75

tcg ccg gag cag ctg cgg gag ctg gag gcc gaa gaa cgc gaa tgg tac 290  
 Ser Pro Glu Gln Leu Arg Glu Leu Glu Ala Glu Glu Arg Glu Trp Tyr  
 80 85 90

ccg agc ctg gcg acc atg cag gag tcg ctg cgg gtg aag cag ctg gcc 338  
 Pro Ser Leu Ala Thr Met Gln Glu Ser Leu Arg Val Lys Gln Leu Ala  
 95 100 105

gaa gag cag aag cgt cgg gag agg gag cag cac atc gca gag tgc atg 386  
 Glu Glu Gln Lys Arg Arg Glu Arg Glu Gln His Ile Ala Glu Cys Met  
 110 115 120 125

gcc aag atg cca cag atg att gtg aac tgg cag cag cag cag ccg gag 434

Ala Lys Met Pro Gln Met Ile Val Asn Trp Gln Gln Gln Gln Arg Glu  
130 135 140

aac tgg gag aag gcc cag gct gac aag gag agg agg gcc cga ctg cag 482  
Asn Trp Glu Lys Ala Gln Ala Asp Lys Glu Arg Arg Ala Arg Leu Gln  
145 150 155

gct gag gcc cag gag ctc ctg ggc tac cag gtg gac cca agg agt gcc 530  
Ala Glu Ala Gln Glu Leu Leu Gly Tyr Gln Val Asp Pro Arg Ser Ala  
160 165 170

cgc ttc cag gag ctg ctc cag gac cta gag aag aag gag cgc aag cgc 578  
Arg Phe Gln Glu Leu Leu Gln Asp Leu Glu Lys Lys Glu Arg Lys Arg  
175 180 185

ctc aag gag gaa aaa cag aaa cgg aag aag gag gcg cga gct gct gca 626  
Leu Lys Glu Glu Lys Gln Lys Arg Lys Lys Glu Ala Arg Ala Ala Ala  
190 195 200 205

ttg gct gca gct gtg gct caa gac cca gca gcc tct ggg gca ccc agc 674  
Leu Ala Ala Ala Val Ala Gln Asp Pro Ala Ala Ser Gly Ala Pro Ser  
210 215 220

tcc tga ggctttgtcc cttcccaata aagcctgcta cctggcagta cccctg 726  
Ser

<210> 154  
<211> 222  
<212> PRT  
<213> Homo sapiens

<400> 154  
Met Ala Ala Ser Val Arg Gln Ala Arg Ser Leu Leu Gly Val Ala Ala  
1 5 10 15  
Thr Leu Ala Pro Gly Ser Arg Gly Tyr Arg Ala Arg Pro Pro Pro Arg  
20 25 30  
Arg Arg Pro Gly Pro Arg Trp Pro Asp Pro Glu Asp Leu Leu Thr Pro  
35 40 45  
Arg Trp Gln Leu Gly Pro Arg Tyr Ala Ala Lys Gln Phe Ala Arg Tyr  
50 55 60  
Gly Ala Ala Ser Gly Val Val Pro Gly Ser Leu Trp Pro Ser Pro Glu  
65 70 75 80  
Gln Leu Arg Glu Leu Glu Ala Glu Glu Arg Glu Trp Tyr Pro Ser Leu  
85 90 95  
Ala Thr Met Gln Glu Ser Leu Arg Val Lys Gln Leu Ala Glu Glu Gln  
100 105 110  
Lys Arg Arg Glu Arg Glu Gln His Ile Ala Glu Cys Met Ala Lys Met  
115 120 125  
Pro Gln Met Ile Val Asn Trp Gln Gln Gln Gln Arg Glu Asn Trp Glu  
130 135 140  
Lys Ala Gln Ala Asp Lys Glu Arg Arg Ala Arg Leu Gln Ala Glu Ala  
145 150 155 160  
Gln Glu Leu Leu Gly Tyr Gln Val Asp Pro Arg Ser Ala Arg Phe Gln  
165 170 175  
Glu Leu Leu Gln Asp Leu Glu Lys Lys Glu Arg Lys Arg Leu Lys Glu  
180 185 190

Glu Lys Gln Lys Arg Lys Lys Glu Ala Arg Ala Ala Ala Leu Ala Ala  
 195 200 205  
 Ala Val Ala Gln Asp Pro Ala Ala Ser Gly Ala Pro Ser Ser  
 210 215 220

<210> 155  
 <211> 1120  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (208)..(1044)

<400> 155  
 cctttttcttc cgcacggttg gaggaggtcg gctggttatc gggagttgga gggctgaggt 60  
 cgggaggggtg gtgtgtacag agctctagga ctcacgcacc aggccagtcg cgggttttgg 120  
 gccgaggcct gggttacaag cagcaagtgc gcggttgggg ccactgagag gccgttttag 180  
 aaaactgttt aaaacaaaga gcaattg atg gat aaa tca gga ata gat tct ctt 234  
 Met Asp Lys Ser Gly Ile Asp Ser Leu  
 1 5  
 gac cat gtg aca tct gat gct gtg gaa ctt gca aat cga agt gat aac 282  
 Asp His Val Thr Ser Asp Ala Val Glu Leu Ala Asn Arg Ser Asp Asn  
 10 15 20 25  
 tct tct gat agc agc tta ttt aaa act cag tgt atc cct tac tca cct 330  
 Ser Ser Asp Ser Ser Leu Phe Lys Thr Gln Cys Ile Pro Tyr Ser Pro  
 30 35 40  
 aaa ggg gag aaa aga aac ccc att cga aaa ttt gtt cgt aca cct gaa 378  
 Lys Gly Glu Lys Arg Asn Pro Ile Arg Lys Phe Val Arg Thr Pro Glu  
 45 50 55  
 agt gtt cac gca agt gat tca tca agt gac tca tct ttt gaa cca ata 426  
 Ser Val His Ala Ser Asp Ser Ser Ser Asp Ser Ser Phe Glu Pro Ile  
 60 65 70  
 cca ttg act ata aaa gct att ttt gaa aga ttc aag aac agg aaa aag 474  
 Pro Leu Thr Ile Lys Ala Ile Phe Glu Arg Phe Lys Asn Arg Lys Lys  
 75 80 85  
 aga tat aaa aaa aag aaa aag agg agg tac cag cca aca gga aga cca 522  
 Arg Tyr Lys Lys Lys Lys Lys Arg Arg Tyr Gln Pro Thr Gly Arg Pro  
 90 95 100 105  
 cgg gga aga cca gaa gga agg aga aat cct ata tac tca cta ata gat 570  
 Arg Gly Arg Pro Glu Gly Arg Arg Asn Pro Ile Tyr Ser Leu Ile Asp  
 110 115 120  
 aag aag aaa caa ttt aga agc aga gga tct ggc ttc cca ttt tta gaa 618  
 Lys Lys Lys Gln Phe Arg Ser Arg Gly Ser Gly Phe Pro Phe Leu Glu  
 125 130 135



65		70		75		80									
Phe	Glu	Arg	Phe	Lys	Asn	Arg	Lys	Lys	Arg	Tyr	Lys	Lys	Lys	Lys	Lys
				85					90					95	
Arg	Arg	Tyr	Gln	Pro	Thr	Gly	Arg	Pro	Arg	Gly	Arg	Pro	Glu	Gly	Arg
			100					105					110		
Arg	Asn	Pro	Ile	Tyr	Ser	Leu	Ile	Asp	Lys	Lys	Lys	Gln	Phe	Arg	Ser
		115					120					125			
Arg	Gly	Ser	Gly	Phe	Pro	Phe	Leu	Glu	Ser	Glu	Asn	Glu	Lys	Asn	Ala
	130					135					140				
Pro	Trp	Arg	Lys	Ile	Leu	Thr	Phe	Glu	Gln	Ala	Val	Ala	Arg	Gly	Phe
145					150					155					160
Phe	Asn	Tyr	Ile	Glu	Lys	Leu	Lys	Tyr	Glu	His	His	Leu	Lys	Glu	Ser
			165					170						175	
Leu	Lys	Gln	Met	Asn	Val	Gly	Glu	Asp	Leu	Glu	Asn	Glu	Asp	Phe	Asp
		180						185					190		
Ser	Arg	Arg	Tyr	Lys	Phe	Leu	Asp	Asp	Asp	Gly	Ser	Ile	Ser	Pro	Ile
	195						200					205			
Glu	Glu	Ser	Thr	Ala	Glu	Asp	Glu	Asp	Ala	Thr	His	Leu	Glu	Asp	Asn
	210					215					220				
Glu	Cys	Asp	Ile	Lys	Leu	Ala	Gly	Asp	Ser	Phe	Ile	Val	Ser	Ser	Glu
225					230					235					240
Phe	Pro	Val	Arg	Leu	Ser	Val	Tyr	Leu	Glu	Glu	Glu	Asp	Ile	Thr	Glu
			245					250						255	
Glu	Ala	Ala	Leu	Ser	Lys	Lys	Arg	Ala	Thr	Lys	Ala	Lys	Asn	Thr	Gly
		260					265						270		
Gln	Arg	Gly	Leu	Lys	Met										
		275													

<210> 157  
 <211> 747  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (27)..(692)

<400> 157  
 ctctctcatg accccgctcc gggatt atg gcc ggg act ggg ctg ctg gcg ctg 53  
 Met Ala Gly Thr Gly Leu Leu Ala Leu  
 1 5

cgg acg ctg cca ggg ccc agc tgg gtg cga ggc tcg ggc cct tcc gtg 101  
 Arg Thr Leu Pro Gly Pro Ser Trp Val Arg Gly Ser Gly Pro Ser Val  
 10 15 20 25

ctg agc cgc ctg cag gac gcg gcc gtg gtg cgg cct ggc ttc ctg agc 149  
 Leu Ser Arg Leu Gln Asp Ala Ala Val Val Arg Pro Gly Phe Leu Ser  
 30 35 40

acg gca gag gag gag acg ctg agc cga gaa ctg gag ccc gag ctg cgc 197  
 Thr Ala Glu Glu Glu Thr Leu Ser Arg Glu Leu Glu Pro Glu Leu Arg  
 45 50 55

cgc cgc cgc tac gaa tac gat cac tgg gac gcg gcc atc cac ggc ttc 245  
 Arg Arg Arg Tyr Glu Tyr Asp His Trp Asp Ala Ala Ile His Gly Phe

60	65	70	
cga gag aca gag aag tcg cgc tgg tca gaa gcc agc cgg gcc atc ctg			293
Arg Glu Thr Glu Lys Ser Arg Trp Ser Glu Ala Ser Arg Ala Ile Leu			
75	80	85	
cag cgc gtg cag gcg gcc gcc ttt ggc ccc ggc cag acc ctg ctc tcc			341
Gln Arg Val Gln Ala Ala Ala Phe Gly Pro Gly Gln Thr Leu Leu Ser			
90	95	100	105
tcc gtg cac gtg ctg gac ctg gaa gcc cgc ggc tac atc aag ccc cac			389
Ser Val His Val Leu Asp Leu Glu Ala Arg Gly Tyr Ile Lys Pro His			
110	115	120	
gtg gac agc atc aag ttc tgc ggg gcc acc atc gcc ggc ctg tct ctc			437
Val Asp Ser Ile Lys Phe Cys Gly Ala Thr Ile Ala Gly Leu Ser Leu			
125	130	135	
ctg tct ccc agc gtt atg cgg ctg gtg cac acc cag gag ccg ggg gag			485
Leu Ser Pro Ser Val Met Arg Leu Val His Thr Gln Glu Pro Gly Glu			
140	145	150	
tgg ctg gaa ctc ttg ctg gag ccg ggc tcc ctc tac atc ctt agg ggc			533
Trp Leu Glu Leu Leu Leu Glu Pro Gly Ser Leu Tyr Ile Leu Arg Gly			
155	160	165	
tca gcc cgt tat gac ttc tcc cat gag atc ctt cgg gat gaa gag tcc			581
Ser Ala Arg Tyr Asp Phe Ser His Glu Ile Leu Arg Asp Glu Glu Ser			
170	175	180	185
ttc ttt ggg gaa cgc cgg att ccc cgg ggc cgg cgc atc tcc gtg atc			629
Phe Phe Gly Glu Arg Arg Ile Pro Arg Gly Arg Arg Ile Ser Val Ile			
190	195	200	
tgc cgc tcc ctc cct gag ggc atg ggg cca ggg gag tct gga cag ccg			677
Cys Arg Ser Leu Pro Glu Gly Met Gly Pro Gly Glu Ser Gly Gln Pro			
205	210	215	
ccc cca gcc tgc tga cccccagctt tctacagaca ccagatttgt gaataaagtt			732
Pro Pro Ala Cys			
220			
ggggaatgga cagcc			747
<210> 158			
<211> 221			
<212> PRT			
<213> Homo sapiens			
<400> 158			
Met Ala Gly Thr Gly Leu Leu Ala Leu Arg Thr Leu Pro Gly Pro Ser			
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Trp Val Arg Gly Ser Gly Pro Ser Val Leu Ser Arg Leu Gln Asp Ala			
20	25	30	
Ala Val Val Arg Pro Gly Phe Leu Ser Thr Ala Glu Glu Glu Thr Leu			
35	40	45	



Gly	Pro	Thr	Ser	Gln	Asp	Thr	Ile	Arg	Asn	Gln	Val	Arg	Lys	Glu	Leu		
			75					80					85				
caa	gcc	gaa	gcc	acc	gtc	agc	ggg	agc	ccc	gag	gcc	cca	ggg	acc	aac	403	
Gln	Ala	Glu	Ala	Thr	Val	Ser	Gly	Ser	Pro	Glu	Ala	Pro	Gly	Thr	Asn		
		90					95					100					
gtg	gta	tct	gag	ccc	aga	gag	gaa	ggc	tct	gcc	cac	ctg	gct	gtg	cct	451	
Val	Val	Ser	Glu	Pro	Arg	Glu	Glu	Gly	Ser	Ala	His	Leu	Ala	Val	Pro		
		105					110				115						
ggc	gtg	tac	ttc	acc	tgt	ccg	ctc	act	ggg	gcc	acc	ctg	agg	aag	gac	499	
Gly	Val	Tyr	Phe	Thr	Cys	Pro	Leu	Thr	Gly	Ala	Thr	Leu	Arg	Lys	Asp		
120					125					130					135		
cag	cgg	gac	gcc	tgc	atc	aag	gag	gcc	att	ctc	ttg	cac	ttc	tcc	acc	547	
Gln	Arg	Asp	Ala	Cys	Ile	Lys	Glu	Ala	Ile	Leu	Leu	His	Phe	Ser	Thr		
			140						145					150			
gac	cca	gtg	gcc	gcc	tcc	atc	atg	aag	atc	tac	acg	ttc	aac	aaa	gac	595	
Asp	Pro	Val	Ala	Ala	Ser	Ile	Met	Lys	Ile	Tyr	Thr	Phe	Asn	Lys	Asp		
		155						160					165				
cag	gac	cgg	gtg	aag	ctg	ggt	gtg	gac	acc	att	gcc	aag	tac	ctg	gac	643	
Gln	Asp	Arg	Val	Lys	Leu	Gly	Val	Asp	Thr	Ile	Ala	Lys	Tyr	Leu	Asp		
		170					175					180					
aac	atc	cac	ctg	cac	ccc	gag	gag	gag	aag	tac	cgg	aag	atc	aag	ctg	691	
Asn	Ile	His	Leu	His	Pro	Glu	Glu	Glu	Lys	Tyr	Arg	Lys	Ile	Lys	Leu		
	185					190				195							
cag	aac	aag	gtg	ttt	cag	gag	cgc	att	aac	tgc	ctg	gaa	ggg	acc	cac	739	
Gln	Asn	Lys	Val	Phe	Gln	Glu	Arg	Ile	Asn	Cys	Leu	Glu	Gly	Thr	His		
200					205				210						215		
gag	ttt	ttt	gag	gcc	att	ggg	ttc	cag	aag	gtg	ttg	ctt	ccc	gcc	cag	787	
Glu	Phe	Phe	Glu	Ala	Ile	Gly	Phe	Gln	Lys	Val	Leu	Leu	Pro	Ala	Gln		
			220					225					230				
gat	cag	gag	gac	ccc	gag	gag	ttc	tac	gtg	ctg	agc	gag	acc	acc	ttg	835	
Asp	Gln	Glu	Asp	Pro	Glu	Glu	Phe	Tyr	Val	Leu	Ser	Glu	Thr	Thr	Leu		
			235					240					245				
gcc	cag	ccc	cag	agc	ctg	gag	agg	cac	aag	gaa	cag	ctg	ctg	gct	gcg	883	
Ala	Gln	Pro	Gln	Ser	Leu	Glu	Arg	His	Lys	Glu	Gln	Leu	Leu	Ala	Ala		
		250					255					260					
gag	ccc	gtg	cgc	gcc	aag	ctg	gac	agg	cag	cgc	cgc	gtc	ttc	cag	ccc	931	
Glu	Pro	Val	Arg	Ala	Lys	Leu	Asp	Arg	Gln	Arg	Arg	Val	Phe	Gln	Pro		
	265					270					275						
tcg	ccc	ctg	gcc	tcg	cag	ttc	gaa	ctg	cct	ggg	gac	ttc	ttc	aac	ctc	979	
Ser	Pro	Leu	Ala	Ser	Gln	Phe	Glu	Leu	Pro	Gly	Asp	Phe	Phe	Asn	Leu		
	280				285					290					295		
aca	gca	gag	gag	atc	aag	cgg	gag	cag	agg	ctc	agg	tcc	gag	gcg	gtg	1027	
Thr	Ala	Glu	Glu	Ile	Lys	Arg	Glu	Gln	Arg	Leu	Arg	Ser	Glu	Ala	Val		

300	305	310	
gag cgg ctg agc gtg ctg cgg acc aag gcc atg cgg gag aag gag gag Glu Arg Leu Ser Val Leu Arg Thr Lys Ala Met Arg Glu Lys Glu Glu 315 320 325			1075
cag cgg ggg ctg cgc aag tac aac tac acg ctg ctg cgc gtg cgc ctc Gln Arg Gly Leu Arg Lys Tyr Asn Tyr Thr Leu Leu Arg Val Arg Leu 330 335 340			1123
ccc gat ggc tgc ctc ctg cag ggc act ttc tac gct cgg gag cgg ctg Pro Asp Gly Cys Leu Leu Gln Gly Thr Phe Tyr Ala Arg Glu Arg Leu 345 350 355			1171
ggg gcg gtg tac ggg ttc gtc cgg gag gcc ctg cag agc gac tgg ctg Gly Ala Val Tyr Gly Phe Val Arg Glu Ala Leu Gln Ser Asp Trp Leu 360 365 370 375			1219
cct ttt gag ctg ctg gcc tcg gga ggg cag aag ctg tcc gag gac gag Pro Phe Glu Leu Leu Ala Ser Gly Gly Gln Lys Leu Ser Glu Asp Glu 380 385 390			1267
aac ctg gcc ttg aac gag tgc ggg ctg gtg ccc tct gcc ctc ctg acc Asn Leu Ala Leu Asn Glu Cys Gly Leu Val Pro Ser Ala Leu Leu Thr 395 400 405			1315
ttc tcg tgg gac atg gct gtg ctg gag gac atc aag gcc gcg ggg gcc Phe Ser Trp Asp Met Ala Val Leu Glu Asp Ile Lys Ala Ala Gly Ala 410 415 420			1363
gag ccg gac tcc atc ctg aaa ccc gag ctc ctg tca gcc atc gag aag Glu Pro Asp Ser Ile Leu Lys Pro Glu Leu Leu Ser Ala Ile Glu Lys 425 430 435			1411
ctc ttg tga aataaaaagca gggttggcct c Leu Leu 440			1441

<210> 160  
 <211> 441  
 <212> PRT  
 <213> Homo sapiens

<400> 160  
 Met Lys Lys Phe Phe Gln Glu Phe Lys Ala Asp Ile Lys Phe Lys Ser  
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 Ala Gly Pro Gly Gln Lys Leu Lys Glu Ser Val Gly Glu Lys Ala His  
 20 25 30  
 Lys Glu Lys Pro Asn Gln Pro Ala Pro Arg Pro Pro Arg Gln Gly Pro  
 35 40 45  
 Thr Asn Glu Ala Gln Met Ala Ala Ala Ala Leu Ala Arg Leu Glu  
 50 55 60  
 Gln Lys Gln Ser Arg Ala Trp Gly Pro Thr Ser Gln Asp Thr Ile Arg  
 65 70 75 80  
 Asn Gln Val Arg Lys Glu Leu Gln Ala Glu Ala Thr Val Ser Gly Ser  
 85 90 95

Pro	Glu	Ala	Pro	Gly	Thr	Asn	Val	Val	Ser	Glu	Pro	Arg	Glu	Glu	Gly	100	105	110
Ser	Ala	His	Leu	Ala	Val	Pro	Gly	Val	Tyr	Phe	Thr	Cys	Pro	Leu	Thr	115	120	125
Gly	Ala	Thr	Leu	Arg	Lys	Asp	Gln	Arg	Asp	Ala	Cys	Ile	Lys	Glu	Ala	130	135	140
Ile	Leu	Leu	His	Phe	Ser	Thr	Asp	Pro	Val	Ala	Ala	Ser	Ile	Met	Lys	145	150	155
Ile	Tyr	Thr	Phe	Asn	Lys	Asp	Gln	Asp	Arg	Val	Lys	Leu	Gly	Val	Asp	165	170	175
Thr	Ile	Ala	Lys	Tyr	Leu	Asp	Asn	Ile	His	Leu	His	Pro	Glu	Glu	Glu	180	185	190
Lys	Tyr	Arg	Lys	Ile	Lys	Leu	Gln	Asn	Lys	Val	Phe	Gln	Glu	Arg	Ile	195	200	205
Asn	Cys	Leu	Glu	Gly	Thr	His	Glu	Phe	Phe	Glu	Ala	Ile	Gly	Phe	Gln	210	215	220
Lys	Val	Leu	Leu	Pro	Ala	Gln	Asp	Gln	Glu	Asp	Pro	Glu	Glu	Phe	Tyr	225	230	235
Val	Leu	Ser	Glu	Thr	Thr	Leu	Ala	Gln	Pro	Gln	Ser	Leu	Glu	Arg	His	245	250	255
Lys	Glu	Gln	Leu	Leu	Ala	Ala	Glu	Pro	Val	Arg	Ala	Lys	Leu	Asp	Arg	260	265	270
Gln	Arg	Arg	Val	Phe	Gln	Pro	Ser	Pro	Leu	Ala	Ser	Gln	Phe	Glu	Leu	275	280	285
Pro	Gly	Asp	Phe	Phe	Asn	Leu	Thr	Ala	Glu	Glu	Ile	Lys	Arg	Glu	Gln	290	295	300
Arg	Leu	Arg	Ser	Glu	Ala	Val	Glu	Arg	Leu	Ser	Val	Leu	Arg	Thr	Lys	305	310	315
Ala	Met	Arg	Glu	Lys	Glu	Glu	Gln	Arg	Gly	Leu	Arg	Lys	Tyr	Asn	Tyr	325	330	335
Thr	Leu	Leu	Arg	Val	Arg	Leu	Pro	Asp	Gly	Cys	Leu	Leu	Gln	Gly	Thr	340	345	350
Phe	Tyr	Ala	Arg	Glu	Arg	Leu	Gly	Ala	Val	Tyr	Gly	Phe	Val	Arg	Glu	355	360	365
Ala	Leu	Gln	Ser	Asp	Trp	Leu	Pro	Phe	Glu	Leu	Leu	Ala	Ser	Gly	Gly	370	375	380
Gln	Lys	Leu	Ser	Glu	Asp	Glu	Asn	Leu	Ala	Leu	Asn	Glu	Cys	Gly	Leu	385	390	395
Val	Pro	Ser	Ala	Leu	Leu	Thr	Phe	Ser	Trp	Asp	Met	Ala	Val	Leu	Glu	405	410	415
Asp	Ile	Lys	Ala	Ala	Gly	Ala	Glu	Pro	Asp	Ser	Ile	Leu	Lys	Pro	Glu	420	425	430
Leu	Leu	Ser	Ala	Ile	Glu	Lys	Leu	Leu								435	440	